GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: May 21, 2003, 17:13:44 ; Search time 34.7838 Seconds
(without alignments)
547.808 Million cell updates/sec

Title: US-09-522-278B-12_COPY_159_301
Perfect score: 738
Sequence: 1 STAPTRSKTPAQGLARKLHF.....PTERPRAPARSASRPRRPVE 143

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002:*
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2: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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22: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	738	100.0	301	19	AAW47194	Herpes simplex vir
2	738	100.0	301	20	AAY42292	Herpes simplex vir
3	738	100.0	301	20	AAY27404	HSV-1 tegument pro
4	738	100.0	301	20	AAW95099	HIV-1 VP22 polypep
5	738	100.0	301	21	AAY83261	HSV-1 V22 cellular
6	738	100.0	301	21	AAY79877	HSV-1 VP22 peptide
7	738	100.0	301	22	AAB60910	HSV-1 VP22 protein
8	738	100.0	301	22	AAB86329	VP22 protein fragm
9	738	100.0	301	22	AAG64275	Herpes simplex vir
10	738	100.0	301	23	ABB05524	HSV-1 VP22 protein
11	738	100.0	418	23	AAU77235	PcDNA3-VP22/E7 fus
12	738	100.0	539	22	AAE05270	Delta VP22Cre-Stre
13	738	100.0	667	22	AAE05266	VP22-Cre fusion pr
14	738	100.0	683	22	AAE05273	VP22CreStrepTag fu
15	738	100.0	747	22	AAE05267	VP22-Flpe fusion p
16	732	99.2	297	21	AAY96574	HSV-1 VP22 polypep
17	596.5	80.8	302	19	AAW72214	HSV-2 strain SB5 C
18	596.5	80.8	306	20	AAW67755	HSV-2 VP22 protein
19	569	77.1	144	19	AAW47195	Herpes simplex vir
20	569	77.1	267	22	AAB86330	VP22 protein fragm
21	471	63.8	117	19	AAW72068	HSV-2 strain SB5 C
22	414.5	56.2	246	21	AAY78333	Herpes simplex vir
23	414.5	56.2	246	23	AAE23170	Herpes simplex vir
24	215.5	29.2	257	15	AAR63461	Deduced AA sequenc
25	210	28.5	258	21	AAB07662	Amino acid sequenc
26	210	28.5	258	23	AAU11367	Bovine herpesvirus
27	189	25.6	249	23	AAU77236	Marek's disease vi
28	184	24.9	249	16	AAR65493	Marek's disease vi
29	179	24.3	37	20	AAW95100	HIV-1 VP22 polypep
30	179	24.3	37	21	AAY96575	HSV-1 VP22 polypep
31	179	24.3	37	21	AAY83262	HSV-1 V22 C-termin
32	179	24.3	37	21	AAY79878	HSV-1 VP22 C-termi
33	179	24.3	37	22	AAB60911	HSV-1 VP22 C-termi
34	179	24.3	37	23	ABB05525	HSV-1 VP22 protein
35	172.5	23.4	139	18	AAW23003	Canine herpesvirus
36	172.5	23.4	139	19	AAW72663	Canine herpes viru
37	172.5	23.4	139	22	AAB51320	Canine herpes viru
38	169	22.9	34	23	AAM48195	Herpes simplex vir
39	166	22.5	34	22	AAE12206	Membrane transport
40	164	22.2	34	23	AAU78347	Herpes simplex-1 v
41	164	22.2	35	23	AAU78354	Herpes simplex-1 v
42	117	15.9	20	19	AAW47198	HSV truncated tegu
43	108	14.6	20	19	AAW47197	HSV truncated tegu
44	106	14.4	20	19	AAW47201	HSV truncated tegu
45	103	14.0	20	19	AAW47200	HSV truncated tegu

ALIGNMENTS

RESULT 1
AAW47194
ID AAW47194 standard; Protein; 301 AA.
XX
AC AAW47194;
XX
DT 03-JUL-1998 (first entry)
XX
DE Herpes simplex virus tegument protein VP22.
XX
KW HSV; tegument protein; VP22; UL49; antiviral agent; treatment;
KW cold sore; genital herpes; chickenpox; shingles.
XX
OS Herpes simplex virus.
XX
PN WO9804708-A1.
XX
PD 05-FEB-1998.
XX
PF 28-JUL-1997; 97WO-GB02036.
XX
PR 26-JUL-1996; 96GB-0015726.
XX
PA (MEDI-) MEDICAL RES COUNCIL.
XX
PI Hope RG, McGeoch DJ, McLaughlan J, Rixon HWM;
XX
DR WPI; 1998-130696/12.
DR N-PSDB; AAV17085.
XX
PT New antiviral agent disrupting binding of VP22 to VP16 or gB -
PT useful for treating infections caused by herpes simplex, e.g. cold
PT sores and chicken-pox

```
XX
PS   Example; Pages 49-50; 75pp; English.
XX
CC   The present sequence is the herpes simplex virus (HSV)
CC   tegument protein VP22. VP22 was used in the preparation of a novel
CC   antiviral agent, which inhibits the maturation and/or replication
CC   of HSV by disrupting association between VP22 and VP16 and/or gB.
CC   The agent can be used to treat, e.g. cold sores, genital herpes,
CC   chickenpox and shingles.
XX
SQ   Sequence   301 AA;

  Query Match            100.0%;  Score 738;  DB 19;  Length 301;
  Best Local Similarity  100.0%;  Pred. No. 7.4e-76;
  Matches  143;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 STAPTRSKTPAQGLARKLHFSTAPPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAV 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    159 STAPTRSKTPAQGLARKLHFSTAPPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAV 218

Qy     61 QLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    219 QLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSA 278

Qy    121 ASRPTERPRAPARSASRPRRPVE 143
          |||||||||||||||||||||||
Db    279 ASRPTERPRAPARSASRPRRPVE 301


RESULT 2
AAY42292
ID   AAY42292 standard; Protein; 301 AA.
XX
AC   AAY42292;
XX
DT   06-DEC-1999  (first entry)
XX
DE   Herpes simplex virus type 1 (HSV-1) VP22 tegument protein.
XX
KW   Cytochrome; targetting; localisation; cancer; tumour; prodrug; reduction;
KW   nucleus.
XX
OS   Herpes simplex virus type 1.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 251..267
FT                   /note= "Corresponding DNA sequence appears to be absent"
XX
PN   WO9945127-A2.
XX
PD   10-SEP-1999.
XX
PF   05-MAR-1999;   99WO-GB00674.
XX
PR   06-MAR-1998;   98GB-0004841.
PR   19-AUG-1998;   98GB-0018103.
PR   29-JAN-1999;   99GB-0002081.
XX
PA   (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI   Stratford IJ,  Patterson AV,  Kingsman SM,  Kan O,  Griffiths L;
PI   Mitrophanous K;
XX
DR   WPI; 1999-551046/46.
DR   N-PSDB; AAZ19784.
XX
PT   New prodrug activating agent targeted to selected cells or tissues,
PT   particularly hypoxic cells, for treating e.g. tumors -
XX
PS   Example 7; Fig 3; 187pp; English.
XX
CC   This sequence represents a Herpes simplex virus type 1 (HSV-1)
CC   VP22 tegument protein, which is involved in transcellular
CC   localisation. VP22 can be fused to cytochrome P450 reductase (P450R)
CC   derivatives such as anchorless P450R (AAY42287) or FN fragment
CC   (AAY42288). This enables the fusion protein to be delivered to
CC   neighbouring cells where it is then transported to the nucleus.  Many
CC   drugs' sites of action are in the nucleus, rather than the cytoplasm,
CC   where P450R normally functions. P450R or its derivatives can be used to
CC   activate prodrugs to their active form via reduction. Administration of a
CC   prodrug is useful where the active drug may be metabolised before it
CC   reaches its site of action or where the active drug is cytotoxic, e.g.,
CC   anticancer drugs. Targetted delivery of such prodrug activators allows a
CC   reduction in dose of the prodrug, and thus of systemic side-effects.
CC   P450R derivative fusion proteins, or vectors that express them, are
CC   specifically used to treat tumours, inflammation, atherosclerosis and
CC   muscular dystrophy, but may also be used to treat many other conditions,
CC   e.g., cerebral malaria, rheumatoid arthritis, or conditions associated
CC   with hypoxia, ischaemia or hypoglycemia, or to deliver antibiotics,
CC   antiviral agents, analgesics, anaesthetics, anti-inflammatories,
CC   antineoplastic agents and diagnostic agents.
XX
SQ   Sequence   301 AA;

  Query Match            100.0%;  Score 738;  DB 20;  Length 301;
  Best Local Similarity  100.0%;  Pred. No. 7.4e-76;
  Matches  143;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 STAPTRSKTPAQGLARKLHFSTAPPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAV 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    159 STAPTRSKTPAQGLARKLHFSTAPPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAV 218

Qy     61 QLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    219 QLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSA 278

Qy    121 ASRPTERPRAPARSASRPRRPVE 143
          |||||||||||||||||||||||
Db    279 ASRPTERPRAPARSASRPRRPVE 301


RESULT 3
AAY27404
ID   AAY27404 standard; Protein; 301 AA.
XX
AC   AAY27404;
XX
DT   23-NOV-1999  (first entry)
XX
DE   HSV-1 tegument protein VP22.
XX
KW   Prodrug; localization domain; tumor-selective antibody; cytochrome P450;
KW   prodrug activating domain; modified hematopoietic stem cell; MHSC; tumor;
KW   inflammation; atherosclerosis; muscular dystrophy; cerebral malaria;
KW   rheumatoid arthritis; hypoxia; ischemia; hypoglycemia; HSV; VP22;
KW   tegument protein.
XX
OS   Herpes simplex virus type 1.
XX
FH   Key             Location/Qualifiers
FT   Region          251..267
FT                   /note= "the corresponding DNA sequence for this region
FT                           is possibly missing; there are only 4 nucleotide
FT                           basepairs indicated as encoding for this entire
FT                           region"
XX
PN   WO9945126-A2.
XX
PD   10-SEP-1999.
XX
PF   05-MAR-1999;   99WO-GB00672.
XX
PR   06-MAR-1998;   98GB-0004841.
PR   19-AUG-1998;   98GB-0018103.
PR   29-JAN-1999;   99GB-0002081.
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XX
PA   (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI   Stratford IJ,  Patterson AV,  Kingsman SM,  Kan O,  Griffiths L;
PI   Mitrophanous K;
XX
DR   WPI; 1999-540852/45.
DR   N-PSDB; AAZ07807.
XX
PT   New prodrug activating agent targeted to selected cells or tissues,
PT   particularly hypoxic cells, for treating e.g. tumors or inflammation -
XX
PS   Example 7; Fig 3D; 149pp; English.
XX
CC   The invention provides a new prodrug activating agent that comprises: (i)
CC   a localization domain (LD; other than a tumor-selective antibody) and a
CC   prodrug activating domain (PAD); (ii) at least one nucleic acid encoding
CC   a cytochrome P450 and under control of at least one constitutive or
CC   inducible expression control sequence or (iii) a modified hematopoietic
CC   stem cell (MHSC) containing at least one nucleic acid encoding a PAD and
CC   under control of elements as in (ii). The prodrug activating agent or
CC   vectors that express them, are specifically used to treat tumors,
CC   inflammation, atherosclerosis and muscular dystrophy, but may also be
CC   used to treat many other conditions, e.g. cerebral malaria, rheumatoid
CC   arthritis, or conditions associated with hypoxia, hypoglycemia or
CC   ischemia, or to deliver antibiotics, antiviral agents, analgesics,
CC   anesthetics, anti-inflammatories, antineoplastic agents and diagnostic
CC   agents. LD optimize activity of PAD, e.g. by delivering it to selected
CC   locations or by delivering it to neighboring cells (bystander effect),
CC   and allow a reduction in dose of prodrug, and thus of systemic side-
CC   effects. Nucleic acids encoding the agent may be expressed selectively
CC   in hypoxic cells. The present sequence represents the HSV-1 tegument
CC   protein VP22. This is used in the construction of a fusion protien
CC   comprising VP22 and a human P450 reductase derivative alP450R.
XX
SQ   Sequence   301 AA;

  Query Match             100.0%;  Score 738;  DB 20;  Length 301;
  Best Local Similarity   100.0%;  Pred. No. 7.4e-76;
  Matches  143;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 STAPTRSKTPAQGLARKLHFSTAPPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAV 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     159 STAPTRSKTPAQGLARKLHFSTAPPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAV 218

Qy      61 QLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     219 QLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSA 278

Qy     121 ASRPTERPRAPARSASRPRRPVE 143
           |||||||||||||||||||||||
Db     279 ASRPTERPRAPARSASRPRRPVE 301


RESULT 4
AAW95099
ID   AAW95099 standard; Protein; 301 AA.
XX
AC   AAW95099;
XX
DT   25-MAY-1999  (first entry)
XX
DE   HIV-1 VP22 polypeptide.
XX
KW   Cyclin-dependent kinase; CDK; CDK/cyclin complex; inhibitory; restenosis;
KW   CDK-binding motif; endothelialisation; fusion protein; therapeutic; acne;
KW   intracellular; transcellular; transcytosis; vascular wound; repair; hair;
KW   smooth muscle; cardiovascular; arteriosclerotic; fibrotic disorder;
KW   cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft;
KW   tumour; inflammation; neurodegeneration; periodontal; spermatogenesis;
KW   tachycardia; HIV-1.
XX
OS   Human immunodeficiency virus type 1.
XX
PN   WO9906540-A2.
XX
PD   11-FEB-1999.
XX
PF   29-JUL-1998;   98WO-US15759.
XX
PR   29-JUL-1997;   97US-0902572.
XX
PA   (MITO-) MITOTIX INC.
XX
PI   Beach DH,  Gyuris J,  Lamphere L;
XX
DR   WPI; 1999-153770/13.
DR   N-PSDB; AAX26227.
XX
PT   Fusion and chimaeric proteins including cyclin-dependent kinase
PT   binding motif - used for regulation of cell proliferation and
PT   differentiation, for treatment of, e.g. vascular injury, cancers,
PT   fibrosis and neurodegeneration
XX
PS   Example 2; Page 26-27; 88pp; English.
XX
CC   The invention relates to novel inhibitors of cyclin-dependent kinases
CC   (CDKs), particularly CDK/cyclin complexes. It provides a recombinant
CC   transfection system (A) that comprises: (i) first gene construct
CC   comprising a sequence encoding an inhibitory polypeptide containing at
CC   least one CDK-binding motif for binding and inhibiting activity of a
CC   CDK, linked to a transcription regulator functional in eukaryotic cells;
CC   (ii) second gene construct comprising a sequence encoding a polypeptide
CC   that promotes endothelialisation, and (iii) a gene delivery composition
CC   for delivering the GCs to a cell for transfection.  Also provided are
CC   nucleic acids encoding a fusion protein (FP) containing: (i) a
CC   therapeutic polypeptide sequence (TP) from an intracellular protein that
CC   alters a cellular process when FP enters the cell, and (ii) a
CC   transcellular polypeptide sequence (TCP) that promotes transcytosis of
CC   FP. The FP consists of at least one CDK-binding motif and a TCP. See
CC   AAX26220 for detailed uses of the recombinant transfection system.  The
CC   CKI polypeptides are engineered to include any of the peptides shown in
CC   AAW95097-100 encoded by the DNA sequences AAX26225-228.
XX
SQ   Sequence   301 AA;

  Query Match             100.0%;  Score 738;  DB 20;  Length 301;
  Best Local Similarity   100.0%;  Pred. No. 7.4e-76;
  Matches  143;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 STAPTRSKTPAQGLARKLHFSTAPPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAV 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     159 STAPTRSKTPAQGLARKLHFSTAPPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAV 218

Qy      61 QLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     219 QLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSA 278

Qy     121 ASRPTERPRAPARSASRPRRPVE 143
           |||||||||||||||||||||||
Db     279 ASRPTERPRAPARSASRPRRPVE 301


RESULT 5
AAY83261
ID   AAY83261 standard; Protein; 301 AA.
XX
AC   AAY83261;
XX
DT   16-AUG-2000  (first entry)
XX
DE   HSV-1 V22 cellular localisation signal sequence.
XX
KW   Ubiquitin ligase; SCF; F-box protein; targeted degradation;
KW   destabilisation; proteolysis; drug discovery; gene therapy; cancer;
KW   oncoprotein; Huntington's disease; gene knockout; delivery systems.
```

```
XX
OS   Synthetic.
OS   Herpes simplex virus-1.
XX
PN   WO200022110-A2.
XX
PD   20-APR-2000.
XX
PF   08-OCT-1999;   99WO-US23705.
XX
PR   09-OCT-1998;   98US-0103787.
XX
PA   (HARD ) HARVARD COLLEGE.
XX
PI   Zhou P,  Howley P;
XX
DR   WPI; 2000-317970/27.
DR   N-PSDB; AAZ93717.
XX
PT   Targeting degradation of polypeptide useful for treating cancer and
PT   other proliferative disorders, involves conjugating polypeptide with
PT   ubiquitin protein ligase or inhibiting ubiquitination using organic
PT   compound
XX
PS   Disclosure; Page 76; 185pp; English.
XX
CC   The F-box proteins are a family of ubiquitin ligases (SCF ubiquitin
CC   ligases) which can be used for the targetted degradation of a target
CC   polypeptide in vivo. Targetted degradation is achieved by expressing
CC   the ubiquitin ligase in a cell linked to the interaction domain of
CC   the target polypeptide and thereby recruiting the target polypeptide
CC   to the ubiquitin ligase. Such methods are useful for decreasing or
CC   increasing the level of a target polypeptide and for creating and
CC   expressing a destabilized polypeptide which is subjected to SCF
CC   mediated proteolysis. Degrading any desired protein in a cell is
CC   useful for preventing or treating diseases caused by the presence of
CC   abnormal amount of the specific polypeptides, for drug discovery and
CC   for gene therapy. Diseases treated include cancer, by degradation of
CC   oncoproteins, Huntington's disease, other proliferative disorders and
CC   microbial infections. The method provides a quick and easy
CC   alternative to gene knockout technology. The target polypeptide can
CC   be degraded at all stages, or a specific stage, of development in the
CC   mature animal. The hybrid ubiquitin ligase may also include an
CC   optional localisation sequence such as this HSV-1 V22 sequence.
XX
SQ   Sequence   301 AA;

  Query Match             100.0%;  Score 738;  DB 21;  Length 301;
  Best Local Similarity   100.0%;  Pred. No. 7.4e-76;
  Matches  143;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 STAPTRSKTPAQGLARKLHFSTAPPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAV 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    159 STAPTRSKTPAQGLARKLHFSTAPPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAV 218

Qy     61 QLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    219 QLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSA 278

Qy    121 ASRPTERPRAPARSASRPRRPVE 143
          |||||||||||||||||||||||
Db    279 ASRPTERPRAPARSASRPRRPVE 301


RESULT 6
AAY79877
ID   AAY79877 standard; Peptide; 301 AA.
XX
AC   AAY79877;
XX
DT   10-MAY-2000  (first entry)
XX
DE   HSV-1 VP22 peptide.
XX
KW   Papillomavirus; PV; infection; cell proliferation; E2; peptidomimetic;
KW   E1; antiviral; virucide; cytostatic; antiproliferative; dermatological;
KW   preneoplastic lesion; neoplastic lesion; cutaneous lesion; wart;
KW   epidermodysplasia verruciformis; anorectal carcinoma.
XX
OS   Herpes simplex virus type 1.
XX
PN   WO200001720-A2.
XX
PD   13-JAN-2000.
XX
PF   02-JUL-1999;   99WO-US15144.
XX
PR   02-JUL-1998;   98US-0091661.
XX
PA   (HARD ) HARVARD COLLEGE.
XX
PI   Howley P,  Benson J,  Kasukawa H;
XX
DR   WPI; 2000-171001/15.
DR   N-PSDB; AAZ88468.
XX
PT   Use of papillomavirus E2 protein peptidomimetics for treating
PT   papillomavirus-infected cells and papillomavirus-induced conditions in
PT   mammals by inhibiting E1-E2 interaction  -
XX
PS   Disclosure; Page 42; 110pp; English.
XX
CC   The present invention describes the use of a small organic compound (A)
CC   which competitively inhibits interaction of a papillomavirus (PV) E2
CC   protein with a PV E1 protein for treating a cell infected with PV or a
CC   mammal with a PV-induced condition. (A) has antiviral, virucide,
CC   cytostatic, antiproliferative and dermatological activities. Methods
CC   from the present invention can be used to treat PV-induced conditions
CC   including growth of PV preneoplastic and neoplastic lesions, cutaneous
CC   lesions chosen from warts and other benign cutaneous lesions, plantar
CC   warts (verruca plantaris), common warts (verruca plana), Butcher's
CC   common warts, flat warts, genital warts (condyloma acuminatum) and
CC   epidermodysplasia verruciformis, laryngeal, oral, pharyngeal,
CC   oesophageal and other upper airway papilloma or vaginal, cervical,
CC   vulvar, penile and anorectal carcinoma. The E2 inhibitors may also be
CC   used to treat epithelial and internal fibropapillomas in animals.
CC   The present sequence represents a peptide sequence used in the
CC   exemplification of the present invention.
XX
SQ   Sequence   301 AA;

  Query Match             100.0%;  Score 738;  DB 21;  Length 301;
  Best Local Similarity   100.0%;  Pred. No. 7.4e-76;
  Matches  143;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 STAPTRSKTPAQGLARKLHFSTAPPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAV 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    159 STAPTRSKTPAQGLARKLHFSTAPPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAV 218

Qy     61 QLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    219 QLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSA 278

Qy    121 ASRPTERPRAPARSASRPRRPVE 143
          |||||||||||||||||||||||
Db    279 ASRPTERPRAPARSASRPRRPVE 301


RESULT 7
AAB60910
ID   AAB60910 standard; Protein; 301 AA.
XX
AC   AAB60910;
XX
DT   05-NOV-2001  (first entry)
XX
```

```
DE   HSV-1 VP22 protein.
XX
KW   Co-activator domain; P300/CBP KIX domain; erythrocythaemia; skin disease;
KW   polycythaemia; haemoglobinopathy; cell differentiation; ulcer; cancer;
KW   neurological condition; neurodegenerative disease; immune disease;
KW   diabetes.
XX
OS   Synthetic.
XX
PN   WO200118036-A2.
XX
PD   15-MAR-2001.
XX
PF   31-AUG-2000; 2000WO-US24010.
XX
PR   03-SEP-1999;   99US-0152402.
XX
PA   (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
PA   (JOSL-) JOSLIN DIABETES CENT INC.
XX
PI   Frangioni JV,  Cantley LC,  Montminy MR;
XX
DR   WPI; 2001-273380/28.
DR   N-PSDB; AAF58996.
XX
PT   Identifying co-activator domain specific transcriptional activators by
PT   contacting a target domain of a selected transcription factor with a
PT   peptide display library, where the identified binding peptides are
PT   useful for reducing hyperglycemia -
XX
PS   Disclosure; Page 78; 156pp; English.
XX
CC   The present invention describes a method of identifying the co-activator
CC   domain of specific synthetic activators, involving contacting the target
CC   domain of a selected transcription factor with a peptide display library,
CC   and identifying those sequences which bind to the target domain. In
CC   particular, those which bind to the KIX domain of P300/CBP are useful.
CC   The peptides can be used in the treatment of diseases related to aberrant
CC   KIX-dependent gene transcription, including erythrocythaemia,
CC   polycythaemia, haemoglobinopathies, to regulate cell differentiation, to
CC   treat neurological diseases, immunological diseases, diabetes, ulcers,
CC   skin diseases and cancer, and to aid wound healing. The present sequence
CC   is a protein described in the exemplification of the invention.
XX
SQ   Sequence   301 AA;

  Query Match             100.0%;  Score 738;  DB 22;  Length 301;
  Best Local Similarity   100.0%;  Pred. No. 7.4e-76;
  Matches  143;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 STAPTRSKTPAQGLARKLHFSTAPPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAV 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    159 STAPTRSKTPAQGLARKLHFSTAPPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAV 218

Qy     61 QLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    219 QLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSA 278

Qy    121 ASRPTERPRAPARSASRPRRPVE 143
          |||||||||||||||||||||||
Db    279 ASRPTERPRAPARSASRPRRPVE 301


RESULT 8
AAB86329
ID   AAB86329 standard; Protein; 301 AA.
XX
AC   AAB86329;
XX
DT   18-SEP-2001  (first entry)
XX
DE   VP22 protein fragment.
XX
KW   Fusion protein; VP22; E7; cell import signal; cell export signal;
KW   antigen; immunization; infection-induced auto-immune disease;
KW   tumor disease.
XX
OS   Unidentified.
XX
PN   WO200151516-A2.
XX
PD   19-JUL-2001.
XX
PF   15-JAN-2001; 2001WO-DE00134.
XX
PR   13-JAN-2000; 2000DE-1001230.
XX
PA   (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
PI   Mueller M,  Michel N,  Osen W,  Gissmann L,  Zentgraf H;
XX
DR   WPI; 2001-442135/47.
XX
PT   Identifying an immunization agent comprising cell import and/or
PT   export signal sequences and an antigen for immunizing against
PT   infection-induced auto-immune and tumor disease  -
XX
PS   Disclosure; Fig 4; 23pp; German.
XX
CC   This invention describes a fusion protein comprising cell import and/or
CC   export signal sequences and an antigen which is suitable for immunizing
CC   an individual against a disease, together with a DNA that codes for said
CC   protein. The invention also relates to the use of the protein (II) and
CC   its encoding DNA (I) for immunizing an individual against diseases, in
CC   particular against infection-induced auto-immune and tumor disease. This
CC   sequence represents the VP22 protein fragment used in the construction of
CC   the fusion construct VP22-E7.
XX
SQ   Sequence   301 AA;

  Query Match             100.0%;  Score 738;  DB 22;  Length 301;
  Best Local Similarity   100.0%;  Pred. No. 7.4e-76;
  Matches  143;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 STAPTRSKTPAQGLARKLHFSTAPPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAV 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    159 STAPTRSKTPAQGLARKLHFSTAPPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAV 218

Qy     61 QLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    219 QLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSA 278

Qy    121 ASRPTERPRAPARSASRPRRPVE 143
          |||||||||||||||||||||||
Db    279 ASRPTERPRAPARSASRPRRPVE 301


RESULT 9
AAG64275
ID   AAG64275 standard; protein; 301 AA.
XX
AC   AAG64275;
XX
DT   21-SEP-2001  (first entry)
XX
DE   Herpes simplex viral protein: SEQ ID 26.
XX
KW   BH4 domain; cardiant; anti-HIV; neuroprotective; hepatotropic; Bcl-2;
KW   antidiabetic; apoptosis inhibitor; cellular uptake; anti-apoptosis;
KW   ischaemic disease; myocardial infarct; AIDS; neurodegenerative diseases;
KW   infective multiple failure; fulminant hepatitis; diabetes.
XX
OS   Herpes simplex virus type 1.
XX
PN   WO200148014-A1.
XX
```

```
PD   05-JUL-2001.
XX
PF   26-DEC-2000; 2000WO-JP09274.
XX
PR   27-DEC-1999;   99JP-0371449.
XX
PA   (SHIO ) SHIONOGI & CO LTD.
XX
PI   Shimizu S,  Tsujimoto Y;
XX
DR   WPI; 2001-418246/44.
XX
PT   BH4-fused polypeptides with peptide sequences capable of exerting
PT   effect on enabling uptake into cells, applicable as effective apoptosis
PT   inhibitors, useful in preventives or remedies for ischemic diseases
PT   e.g. myocardial infarct -
XX
PS   Claim 5; Page 74-6; 84pp; Japanese.
XX
CC   The present invention relates to BH4-fused polypeptides. The BH4-fused
CC   polypeptide have a sequence capable of affecting cellular uptake and also
CC   a BH4 domain sequence from an anti-apoptosis Bcl-2 family protein. The
CC   BH4-fused polypeptides are useful as effective apoptosis inhibitors, and
CC   are useful in preventives or remedies for ischaemic diseases e.g.
CC   myocardial infarct, AIDS, neurodegenerative diseases, infective multiple
CC   failure, fulminant hepatitis and diabetes. The present peptide was used
CC   in the present invention.
XX
SQ   Sequence   301 AA;

  Query Match             100.0%;  Score 738;  DB 22;  Length 301;
  Best Local Similarity   100.0%;  Pred. No. 7.4e-76;
  Matches  143;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 STAPTRSKTPAQGLARKLHFSTAPPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAV 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    159 STAPTRSKTPAQGLARKLHFSTAPPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAV 218

Qy     61 QLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    219 QLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSA 278

Qy    121 ASRPTERPRAPARSASRPRRPVE 143
          |||||||||||||||||||||||
Db    279 ASRPTERPRAPARSASRPRRPVE 301


RESULT 10
ABB05524
ID   ABB05524 standard; Protein; 301 AA.
XX
AC   ABB05524;
XX
DT   22-APR-2002  (first entry)
XX
DE   HSV-1 VP22 protein.
XX
KW   Ubiquitin dependent proteolysis modulation; cdc4 phospho design motif;
KW   CDP motif; cytostatic; nootropic; antiproliferative; cell proliferation;
KW   growth; differentiation; cancer; neurodegenerative disorder;
KW   spinal degeneration.
XX
OS   Herpes simplex virus.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 125
FT                   /note= "encoded by CAG"
XX
PN   WO200183518-A2.
XX
PD   08-NOV-2001.
XX
PF   04-MAY-2001; 2001WO-CA00632.
XX
PR   04-MAY-2000; 2000US-202166P.
PR   24-JAN-2001; 2001US-263774P.
XX
PA   (MOUN ) MOUNT SINAI HOSPITAL.
XX
PI   Nash P,  Pawson T,  Tang X,  Tyers M;
XX
DR   WPI; 2002-164074/21.
DR   N-PSDB; ABA93386.
XX
PT   New Cdc4 Phospho Design motif that targets molecules for ubiquitin
PT   dependent proteolysis, is useful for the modulation of cell
PT   proliferation i.e. cancer treatment -
XX
PS   Disclosure; Page 30; 83pp; English.
XX
CC   The present invention describes a cdc4 phospho design (CPD) motif, (C),
CC   that targets molecules for ubiquitin dependent proteolysis. (C) have
CC   cytostatic, nootropic and antiproliferative activity. Also described is
CC   a method for the treatment of a disease or condition where affected
CC   cells have a defective protein, comprising administering (C) to promote
CC   degradation of the target protein in cells by ubiquitin dependent
CC   proteolysis. (C) can also be used for modulating the proliferation,
CC   growth and/or differentiation of cells. (C) can be used to modulate
CC   ubiquitin dependent proteolysis or cell proliferation, growth and or
CC   differentiation of cells. (C) is useful in the treatment of cancers and
CC   neurodegenerative disorders as well as spinal degeneration. The present
CC   sequence represents the HSV-1 VP22 protein which is given in the
CC   exemplification of the present invention.
XX
SQ   Sequence   301 AA;

  Query Match             100.0%;  Score 738;  DB 23;  Length 301;
  Best Local Similarity   100.0%;  Pred. No. 7.4e-76;
  Matches  143;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 STAPTRSKTPAQGLARKLHFSTAPPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAV 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    159 STAPTRSKTPAQGLARKLHFSTAPPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAV 218

Qy     61 QLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    219 QLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSA 278

Qy    121 ASRPTERPRAPARSASRPRRPVE 143
          |||||||||||||||||||||||
Db    279 ASRPTERPRAPARSASRPRRPVE 301


RESULT 11
AAU77235
ID   AAU77235 standard; Protein; 418 AA.
XX
AC   AAU77235;
XX
DT   05-JUN-2002  (first entry)
XX
DE   PcDNA3-VP22/E7 fusion protein sequence.
XX
KW   Virucide; cytostatic; vaccine; intercellular transport; antigenic;
KW   immune response; cytotoxic T lymphocyte; tumour; cancer; pcDNA3-VP22/E7;
KW   chronic viral infection; veterinary herpesvirus infection; pseudorabies;
KW   equine herpesvirus; bovine herpesvirus; Marek's disease virus; chicken;
KW   fowl; animal retroviral disease; rabies; fusion protein.
XX
OS   Chimeric - herpes simplex virus type 1.
OS   Chimeric - human papilloma virus type 16.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Protein         1..301
FT                   /note= "VP22 transport polypeptide from herpes simplex
```

```
FT                      virus type 1, specifically claimed in claim 10"
FT   Region          302..307
FT                   /note= "Linker sequence"
FT   Protein         308..403
FT                   /note= "Represents 96 of the 98 residues of E7 from
FT                         human papilloma virus type 16"
FT   Region          404..418
FT                   /note= "Vector sequence"
XX
PN   WO200209645-A2.
XX
PD   07-FEB-2002.
XX
PF   01-AUG-2001; 2001WO-US23966.
XX
PR   01-AUG-2000; 2000US-222185P.
PR   15-FEB-2001; 2001US-268575P.
PR   04-APR-2001; 2001US-281004P.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Wu T,  Hung C;
XX
DR   WPI; 2002-257367/30.
DR   N-PSDB; ABK11810.
XX
PT   New nucleic acids encoding fusion polypeptide comprising intercellular
PT   transport polypeptide linked to antigenic polypeptide, useful as
PT   therapeutic vaccine for cancer and major chronic viral infections -
XX
PS   Disclosure; Fig 7; 102pp; English.
XX
CC   The present invention relates to a new nucleic acid molecule that
CC   encodes a fusion polypeptide. The fusion protein comprises a first
CC   polypeptide comprising at least one intercellular transport polypeptide
CC   and a second polypeptide comprising at least one antigenic polypeptide
CC   or peptide. The invention also describes an optional linker peptide
CC   linking the first and second polypeptide. The nucleic acid is useful as
CC   a vaccine for enhancing immune responses, primarily cytotoxic T
CC   lymphocyte responses to specific antigens such as tumour or viral
CC   antigens. The compositions comprising the nucleic acids are especially
CC   useful as a therapeutic vaccine for cancer and for major chronic viral
CC   infections, as well as in the treatment of veterinary herpesvirus
CC   infections, including equine or bovine herpesvirus, Marek's disease virus
CC   in chickens and other fowls, animal retroviral diseases, pseudorabies
CC   and rabies. The present amino acid sequence represents the pcDNA3-VP22/E7
CC   fusion protein of the invention.
XX
SQ   Sequence   418 AA;

  Query Match             100.0%;  Score 738;  DB 23;  Length 418;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-75;
  Matches  143;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 STAPTRSKTPAQGLARKLHFSTAPPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAV 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     159 STAPTRSKTPAQGLARKLHFSTAPPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAV 218

Qy      61 QLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSA 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     219 QLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSA 278

Qy     121 ASRPTERPRAPARSASRPRRPVE 143
           |||||||||||||||||||||||
Db     279 ASRPTERPRAPARSASRPRRPVE 301


RESULT 12
AAE05270
ID   AAE05270 standard; Protein; 539 AA.
XX
AC   AAE05270;
XX
DT   12-SEP-2001  (first entry)
XX
DE   Delta VP22Cre-StrepTag fusion protein.
XX
KW   DNA recombinase domain; protein transduction domain; PTD;
KW   gene alteration; delta VP22Cre-StrepTag fusion protein;
KW   Human immunodeficiency virus; HIV; Human spumaretrovirus; HSV.
XX
OS   Chimeric - Human spumaretrovirus.
OS   Chimeric - Unidentified.
XX
PN   WO200149832-A2.
XX
PD   12-JUL-2001.
XX
PF   05-JAN-2001; 2001WO-EP00060.
XX
PR   07-JAN-2000; 2000EP-0100351.
PR   10-NOV-2000; 2000EP-0124595.
XX
PA   (ARTE-) ARTEMIS PHARM GMBH.
XX
PI   Schwenk F;
XX
DR   WPI; 2001-441873/47.
DR   N-PSDB; AAD09263.
XX
PT   Using site-specific DNA recombinase domain/protein transduction domain
PT   fusion proteins for inducing target gene alterations in organisms or
PT   cell cultures -
XX
PS   Claim 6; Page 46-47; 85pp; English.
XX
CC   The present invention relates to use of fusion proteins comprising
CC   a site-specific DNA recombinase domain e.g. Cre and a protein
CC   transduction domain (PTD) e.g. the Human immunodeficiency virus
CC   (HIV) derived TAT peptide, for preparing an agent for inducing
CC   target gene alterations in a living organism or cell culture. The
CC   present invention also provides a method for inducing gene
CC   alterations in living organisms using the fusion proteins of the
CC   invention. The present sequence is delta VP22Cre-StrepTag fusion
CC   protein. The VP22 sequence is from Human spumaretrovirus (HSV).
XX
SQ   Sequence   539 AA;

  Query Match             100.0%;  Score 738;  DB 22;  Length 539;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-75;
  Matches  143;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 STAPTRSKTPAQGLARKLHFSTAPPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAV 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      15 STAPTRSKTPAQGLARKLHFSTAPPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAV 74

Qy      61 QLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSA 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      75 QLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSA 134

Qy     121 ASRPTERPRAPARSASRPRRPVE 143
           |||||||||||||||||||||||
Db     135 ASRPTERPRAPARSASRPRRPVE 157


RESULT 13
AAE05266
ID   AAE05266 standard; Protein; 667 AA.
XX
AC   AAE05266;
XX
DT   12-SEP-2001  (first entry)
XX
DE   VP22-Cre fusion protein.
XX
KW   DNA recombinase domain; protein transduction domain; PTD;
```

```
KW   gene alteration; VP22-Cre fusion protein; Human immunodeficiency virus;
KW   HIV; Human spumaretrovirus; HSV.
XX
OS   Chimeric - Human spumaretrovirus.
OS   Chimeric - Unidentified.
XX
PN   WO200149832-A2.
XX
PD   12-JUL-2001.
XX
PF   05-JAN-2001; 2001WO-EP00060.
XX
PR   07-JAN-2000; 2000EP-0100351.
PR   10-NOV-2000; 2000EP-0124595.
XX
PA   (ARTE-) ARTEMIS PHARM GMBH.
XX
PI   Schwenk F;
XX
DR   WPI; 2001-441873/47.
DR   N-PSDB; AAD09259.
XX
PT   Using site-specific DNA recombinase domain/protein transduction domain
PT   fusion proteins for inducing target gene alterations in organisms or
PT   cell cultures -
XX
PS   Claim 12; Page 35-37; 85pp; English.
XX
CC   The present invention relates to use of fusion proteins comprising
CC   a site-specific DNA recombinase domain e.g. Cre and a protein
CC   transduction domain (PTD) e.g. the Human immunodeficiency virus
CC   (HIV) derived TAT peptide, for preparing an agent for inducing
CC   target gene alterations in a living organism or cell culture. The
CC   present invention also provides a method for inducing gene
CC   alterations in living organisms using the fusion proteins of the
CC   invention. The present sequence is VP22-Cre fusion protein. The
CC   VP22 sequence is from Human spumaretrovirus (HSV).
XX
SQ   Sequence   667 AA;

  Query Match             100.0%;  Score 738;  DB 22;  Length 667;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-75;
  Matches  143;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 STAPTRSKTPAQGLARKLHFSTAPPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAV 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    159 STAPTRSKTPAQGLARKLHFSTAPPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAV 218

Qy     61 QLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    219 QLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSA 278

Qy    121 ASRPTERPRAPARSASRPRRPVE 143
          |||||||||||||||||||||||
Db    279 ASRPTERPRAPARSASRPRRPVE 301


RESULT 14
AAE05273
ID   AAE05273 standard; Protein; 683 AA.
XX
AC   AAE05273;
XX
DT   12-SEP-2001  (first entry)
XX
DE   VP22CreStrepTag fusion protein.
XX
KW   DNA recombinase domain; protein transduction domain; PTD;
KW   VP22CreStrepTag fusion protein; Human immunodeficiency virus; HIV;
KW   gene alteration; Human spumaretrovirus; HSV.
XX
OS   Chimeric - Human spumaretrovirus.
OS   Chimeric - Unidentified.
XX
PN   WO200149832-A2.
XX
PD   12-JUL-2001.
XX
PF   05-JAN-2001; 2001WO-EP00060.
XX
PR   07-JAN-2000; 2000EP-0100351.
PR   10-NOV-2000; 2000EP-0124595.
XX
PA   (ARTE-) ARTEMIS PHARM GMBH.
XX
PI   Schwenk F;
XX
DR   WPI; 2001-441873/47.
DR   N-PSDB; AAD09268.
XX
PT   Using site-specific DNA recombinase domain/protein transduction domain
PT   fusion proteins for inducing target gene alterations in organisms or
PT   cell cultures -
XX
PS   Disclosure; Page 58-60; 85pp; English.
XX
CC   The present invention relates to use of fusion proteins comprising
CC   a site-specific DNA recombinase domain e.g. Cre and a protein
CC   transduction domain (PTD) e.g. the Human immunodeficiency virus
CC   (HIV) derived TAT peptide, for preparing an agent for inducing
CC   target gene alterations in a living organism or cell culture. The
CC   present invention also provides a method for inducing gene
CC   alterations in living organisms using the fusion proteins of the
CC   invention. The present sequence is VP22CreStrepTag fusion protein.
CC   The VP22 sequence is from Human spumaretrovirus (HSV).
XX
SQ   Sequence   683 AA;

  Query Match             100.0%;  Score 738;  DB 22;  Length 683;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-75;
  Matches  143;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 STAPTRSKTPAQGLARKLHFSTAPPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAV 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    159 STAPTRSKTPAQGLARKLHFSTAPPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAV 218

Qy     61 QLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    219 QLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSA 278

Qy    121 ASRPTERPRAPARSASRPRRPVE 143
          |||||||||||||||||||||||
Db    279 ASRPTERPRAPARSASRPRRPVE 301


RESULT 15
AAE05267
ID   AAE05267 standard; Protein; 747 AA.
XX
AC   AAE05267;
XX
DT   12-SEP-2001  (first entry)
XX
DE   VP22-Flpe fusion protein.
XX
KW   DNA recombinase domain; protein transduction domain; PTD;
KW   gene alteration; VP22-Flpe fusion protein; Human immunodeficiency virus;
KW   HIV; Human spumaretrovirus; HSV.
XX
OS   Chimeric - Human spumaretrovirus.
OS   Chimeric - Unidentified.
XX
PN   WO200149832-A2.
XX
PD   12-JUL-2001.
XX
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PF 05-JAN-2001; 2001WO-EP00060.
XX
PR 07-JAN-2000; 2000EP-0100351.
PR 10-NOV-2000; 2000EP-0124595.
XX
PA (ARTE-) ARTEMIS PHARM GMBH.
XX
PI Schwenk F;
XX
DR WPI; 2001-441873/47.
DR N-PSDB; AAD09260.
XX
PT Using site-specific DNA recombinase domain/protein transduction domain
PT fusion proteins for inducing target gene alterations in organisms or
PT cell cultures -
XX
PS Claim 12; Page 40-43; 85pp; English.
XX
CC The present invention relates to use of fusion proteins comprising
CC a site-specific DNA recombinase domain e.g. Cre and a protein
CC transduction domain (PTD) e.g. the Human immunodeficiency virus
CC (HIV) derived TAT peptide, for preparing an agent for inducing
CC target gene alterations in a living organism or cell culture. The
CC present invention also provides a method for inducing gene
CC alterations in living organisms using the fusion proteins of the
CC invention. The present sequence is VP22-Flpe fusion protein. The
CC VP22 sequence is from Human spumaretrovirus (HSV).
XX
SQ Sequence 747 AA;

Query Match 100.0%; Score 738; DB 22; Length 747;
Best Local Similarity 100.0%; Pred. No. 2.5e-75;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      61 QLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSA 120
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Db     219 QLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSA 278

Qy     121 ASRPTERPRAPARSASRPRRPVE 143
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Db     279 ASRPTERPRAPARSASRPRRPVE 301
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Job time : 35.7838 secs

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GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: May 21, 2003, 17:33:24 ; Search time 12.2387 Seconds
(without alignments)
343.784 Million cell updates/sec

Title: US-09-522-278B-12_COPY_159_301
Perfect score: 738
Sequence: 1 STAPTRSKTPAQGLARKLHF.....PTERPRAPARSASRPRRPVE 143

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	738	100.0	301	3	US-08-303-861-21	Sequence 21, Appl
2	738	100.0	301	4	US-09-011-073A-1	Sequence 1, Appli
3	738	100.0	301	4	US-09-347-504-12	Sequence 12, Appl
4	730	98.9	301	4	US-09-230-421-2	Sequence 2, Appli
5	569	77.1	144	4	US-09-230-421-3	Sequence 3, Appli
6	414.5	56.2	246	4	US-09-336-093-5	Sequence 5, Appli
7	210	28.5	258	3	US-08-303-861-18	Sequence 18, Appl
8	210	28.5	258	3	US-08-303-861-19	Sequence 19, Appl
9	210	28.5	258	4	US-09-213-343-2	Sequence 2, Appli
10	205	27.8	302	3	US-08-303-861-20	Sequence 20, Appl
11	179	24.3	37	4	US-09-347-504-14	Sequence 14, Appl
12	172.5	23.4	139	1	US-08-680-726A-66	Sequence 66, Appl
13	172.5	23.4	139	4	US-09-092-409-66	Sequence 66, Appl
14	169	22.9	34	4	US-09-011-073A-2	Sequence 2, Appli
15	166	22.5	32	4	US-09-230-421-14	Sequence 14, Appl
16	117	15.9	20	4	US-09-230-421-6	Sequence 6, Appli
17	108	14.6	20	4	US-09-230-421-5	Sequence 5, Appli
18	106	14.4	20	4	US-09-230-421-9	Sequence 9, Appli
19	103	14.0	20	4	US-09-230-421-7	Sequence 7, Appli
20	103	14.0	20	4	US-09-230-421-8	Sequence 8, Appli
21	100	13.6	20	4	US-09-230-421-11	Sequence 11, Appl
22	99	13.4	20	4	US-09-230-421-10	Sequence 10, Appl
23	90.5	12.3	1996	2	US-08-804-227C-9	Sequence 9, Appli
24	90.5	12.3	1996	2	US-08-804-198-3	Sequence 3, Appli
25	89	12.1	20	4	US-09-230-421-12	Sequence 12, Appl
26	80.5	10.9	2205	1	US-08-093-453B-2	Sequence 2, Appli
27	72.5	9.8	1110	1	US-08-118-441-29	Sequence 29, Appl
28	72.5	9.8	1110	3	US-08-338-579A-29	Sequence 29, Appl
29	72.5	9.8	1110	5	PCT-US94-09851-29	Sequence 29, Appl
30	70	9.5	20	4	US-09-230-421-4	Sequence 4, Appli
31	70	9.5	564	4	US-09-211-704A-8	Sequence 8, Appli
32	70	9.5	669	3	US-08-704-711A-3	Sequence 3, Appli
33	70	9.5	669	4	US-09-521-220-3	Sequence 3, Appli
34	70	9.5	669	4	US-09-391-104-29	Sequence 29, Appl
35	70	9.5	2890	4	US-09-413-814-67	Sequence 67, Appl
36	70	9.5	3798	3	US-09-335-409-6	Sequence 6, Appli
37	70	9.5	3798	4	US-09-568-102-6	Sequence 6, Appli
38	70	9.5	3798	4	US-09-567-969-6	Sequence 6, Appli
39	70	9.5	3798	4	US-09-568-480-6	Sequence 6, Appli
40	70	9.5	3798	4	US-09-568-486-6	Sequence 6, Appli
41	70	9.5	3798	4	US-09-568-472-6	Sequence 6, Appli
42	70	9.5	3798	4	US-09-567-899-6	Sequence 6, Appli
43	68.5	9.3	492	4	US-09-724-864-39	Sequence 39, Appl
44	68.5	9.3	1626	2	US-08-771-602D-2	Sequence 2, Appli
45	68.5	9.3	1626	4	US-09-232-446B-2	Sequence 2, Appli

ALIGNMENTS

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RESULT 1
US-08-303-861-21
; Sequence 21, Application US/08303861
; Patent No. 6086902
;  GENERAL INFORMATION:
;    APPLICANT:  ZAMB, TIMOTHY
;    APPLICANT:  LIANG, XIAOPING
;    APPLICANT:  BABIUK, LORNE A.
;    TITLE OF INVENTION:  RECOMBINANT BOVINE HERPESVIRUS TYPE I
;    TITLE OF INVENTION:  VACCINES
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  755 Page Mill Road
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304-1018
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/303,861
;      FILING DATE:  09-SEP-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  PARK, FREDDIE K.
;      REGISTRATION NUMBER:  35,636
;      REFERENCE/DOCKET NUMBER:  29310-20020.20
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 813-5600
;      TELEFAX:  (415) 494-0792
;      TELEX:  706141
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  301 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-303-861-21

  Query Match             100.0%;  Score 738;  DB 3;  Length 301;
  Best Local Similarity   100.0%;  Pred. No. 4e-79;
  Matches  143;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db    219 QLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSA 278

Qy    121 ASRPTERPRAPARSASRPRRPVE 143
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Db    279 ASRPTERPRAPARSASRPRRPVE 301


RESULT 2
US-09-011-073A-1
; Sequence 1, Application US/09011073A
; Patent No. 6184038
;  GENERAL INFORMATION:
;    APPLICANT:  O'Hare et al.
;    TITLE OF INVENTION:  TRANSPORT PROTEINS AND THEIR USES
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Klarquist Sparkman Campbell Leigh &
;      ADDRESSEE:  Whinston, LLP
;      STREET:  One World Trade Center
;      STREET:  121 S.W. Salmon Street
;      STREET:  Suite 1600
;      CITY:  Portland
;      STATE:  Oregon
;      COUNTRY:  United States of America
;      ZIP:  97204-2988
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Disk, 3-1/2 inch
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  MS DOS
;      SOFTWARE:  WordPerfect 7.0 & ASCII
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,073A
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB96/01831
;      FILING DATE:  JULY 25, 1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Earp, David J.
;      REGISTRATION NUMBER:  41,401
;      REFERENCE/DOCKET NUMBER:  5759-49294/DJE
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (503) 226-7391
;      TELEFAX:  (503) 228-9446
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  301
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-011-073A-1

  Query Match             100.0%;  Score 738;  DB 4;  Length 301;
  Best Local Similarity   100.0%;  Pred. No. 4e-79;
  Matches  143;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy     61 QLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSA 120
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Db    219 QLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSA 278

Qy    121 ASRPTERPRAPARSASRPRRPVE 143
          |||||||||||||||||||||||
Db    279 ASRPTERPRAPARSASRPRRPVE 301


RESULT 3
US-09-347-504-12
; Sequence 12, Application US/09347504
; Patent No. 6399075
; GENERAL INFORMATION:
;  APPLICANT:  Howley, Peter M.
;  APPLICANT:  Benson, John
;  APPLICANT:  Kasukawa, Hiroaki
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR TREATING
;  TITLE OF INVENTION:  PAPILLOMAVIRUS-INFECTED CELLS
;  FILE REFERENCE:  HMV-041.01
;  CURRENT APPLICATION NUMBER: US/09/347,504
;  CURRENT FILING DATE:  1999-07-02
;  NUMBER OF SEQ ID NOS:  79
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 12
;   LENGTH: 301
;   TYPE: PRT
;   ORGANISM: HSV
;   FEATURE:
;   OTHER INFORMATION: HSV-1 VP22 peptide
US-09-347-504-12

  Query Match             100.0%;  Score 738;  DB 4;  Length 301;
  Best Local Similarity   100.0%;  Pred. No. 4e-79;
  Matches  143;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 STAPTRSKTPAQGLARKLHFSTAPPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAV 60
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Db    159 STAPTRSKTPAQGLARKLHFSTAPPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAV 218

Qy     61 QLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSA 120
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Db    219 QLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSA 278

Qy    121 ASRPTERPRAPARSASRPRRPVE 143
          |||||||||||||||||||||||
Db    279 ASRPTERPRAPARSASRPRRPVE 301


RESULT 4
US-09-230-421-2
; Sequence 2, Application US/09230421
; Patent No. 6200577
; GENERAL INFORMATION:
;  APPLICANT:  Medical Research Council
;  TITLE OF INVENTION:  ANTI-HERPESVIRAL ALENTS AND ASSAYS
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE:  P18189C
;  CURRENT APPLICATION NUMBER: US/09/230,421
;  CURRENT FILING DATE:  1999-01-25
;  NUMBER OF SEQ ID NOS:  14
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 2
;   LENGTH: 301
;   TYPE: PRT
;   ORGANISM: HERPESVIRUS TYPE 1
US-09-230-421-2

  Query Match             98.9%;  Score 730;  DB 4;  Length 301;
  Best Local Similarity   99.3%;  Pred. No. 3.5e-78;
  Matches  142;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Qy     61 QLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSA 120
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Db    219 QLWDMSRPRTDEALNELLGITTIRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSA 278

Qy    121 ASRPTERPRAPARSASRPRRPVE 143
          |||||||||||||||||||||||
Db    279 ASRPTERPRAPARSASRPRRPVE 301
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RESULT 5
US-09-230-421-3
; Sequence 3, Application US/09230421
; Patent No. 6200577
; GENERAL INFORMATION:
;  APPLICANT: Medical Research Council
;  TITLE OF INVENTION:  ANTI-HERPESVIRAL ALENTS AND ASSAYS
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE:  P18189C
;  CURRENT APPLICATION NUMBER: US/09/230,421
;  CURRENT FILING DATE:  1999-01-25
;  NUMBER OF SEQ ID NOS:  14
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 3
;   LENGTH: 144
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC PEPTIDES DERIVED FROM THE VP22TRUNC
;   OTHER INFORMATION: SEQUENCE
US-09-230-421-3

  Query Match             77.1%;  Score 569;  DB 4;  Length 144;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-59;
  Matches  109;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      23 STAPTRSKTPAQGLARKLHFSTAPPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAV 82

Qy      61 QLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQDV 109
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Db      83 QLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQDV 131


RESULT 6
US-09-336-093-5
; Sequence 5, Application US/09336093A
; Patent No. 6348185
; GENERAL INFORMATION:
;  APPLICANT: Washington University School of Medicine
;  TITLE OF INVENTION: MEMBRANE-PERMEANT PEPTIDE COMPLEXES FOR MEDICAL
;  TITLE OF INVENTION: IMAGING, DIAGNOSTICS, AND PHARMACEUTICAL THERAPY
;  FILE REFERENCE: WSHU 2001
;  CURRENT APPLICATION NUMBER: US/09/336,093A
;  CURRENT FILING DATE: 1999-06-18
;  NUMBER OF SEQ ID NOS: 31
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 246
;   TYPE: PRT
;   ORGANISM: Herpes simplex virus VP22 protein
US-09-336-093-5

  Query Match             56.2%;  Score 414.5;  DB 4;  Length 246;
  Best Local Similarity   64.3%;  Pred. No. 4.8e-41;
  Matches   99;  Conservative    3;  Mismatches   33;  Indels   19;  Gaps    5;

Qy       4 PTRSKTPAQGLARKLHFSTAPPNPDAPWTPRVAGFNKRVFCAAV----GRLAAM------ 53
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Db      98 PARAPPPPAGSGGAGRTPTTAPR--APRTQRVA--TKAPAAPAAETTRGRKSAQPESAAL 153

Qy      54 ----HARMAAVQLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQDV 109
               :|   |||| ||||||||||||||||  ||||||||||||||||||||||||||||
Db     154 PDAPASRAPTVQLWQMSRPRTDEDLNELLGITH-RVTVCEGKNLLQRANELVNPDVVQDV 212

Qy     110 DAATATRGRSAASRPTERPRAPARSASRPRRPVE 143
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Db     213 DAATATRGRSAASRPTERPRAPARSASRPRRPVE 246


RESULT 7
US-08-303-861-18
; Sequence 18, Application US/08303861
; Patent No. 6086902
;  GENERAL INFORMATION:
;    APPLICANT:  ZAMB, TIMOTHY
;    APPLICANT:  LIANG, XIAOPING
;    APPLICANT:  BABIUK, LORNE A.
;    TITLE OF INVENTION:  RECOMBINANT BOVINE HERPESVIRUS TYPE I
;    TITLE OF INVENTION:  VACCINES
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  755 Page Mill Road
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304-1018
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/303,861
;      FILING DATE:  09-SEP-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  PARK, FREDDIE K.
;      REGISTRATION NUMBER:  35,636
;      REFERENCE/DOCKET NUMBER:  29310-20020.20
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 813-5600
;      TELEFAX:  (415) 494-0792
;      TELEX:  706141
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  258 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-303-861-18

  Query Match             28.5%;  Score 210;  DB 3;  Length 258;
  Best Local Similarity   34.1%;  Pred. No. 7.2e-17;
  Matches   45;  Conservative   20;  Mismatches   63;  Indels    4;  Gaps    1;

Qy       1 STAPTRSKTP----AQGLARKLHFSTAPPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHAR 56
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Db     127 AVGPPRPRAPPGANAVASGRPLAFSAAPKTPKAPWCGPTHAYNRTIFCEAVALVAAEYAR 186

Qy      57 MAAVQLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQDVDAATATR 116
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Db     187 QAAASVWDSDPPKSNERLDRMLKSAAIRILVCEGSGLLAAANDILAARAQRPAARGSTSG 246

Qy     117 GRSAASRPTERP 128
           | |       ||
Db     247 GESRLRGERARP 258


RESULT 8
US-08-303-861-19
; Sequence 19, Application US/08303861
; Patent No. 6086902
;  GENERAL INFORMATION:
;    APPLICANT:  ZAMB, TIMOTHY
;    APPLICANT:  LIANG, XIAOPING
;    APPLICANT:  BABIUK, LORNE A.
;    TITLE OF INVENTION:  RECOMBINANT BOVINE HERPESVIRUS TYPE I
;    TITLE OF INVENTION:  VACCINES
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
```

```
;       STREET:  755 Page Mill Road
;       CITY:  Palo Alto
;       STATE:  California
;       COUNTRY:  USA
;       ZIP:  94304-1018
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/303,861
;       FILING DATE:  09-SEP-1994
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  PARK, FREDDIE K.
;       REGISTRATION NUMBER:  35,636
;       REFERENCE/DOCKET NUMBER:  29310-20020.20
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (415) 813-5600
;       TELEFAX:  (415) 494-0792
;       TELEX:  706141
;   INFORMATION FOR SEQ ID NO:  19:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  258 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-303-861-19

  Query Match             28.5%;  Score 210;  DB 3;  Length 258;
  Best Local Similarity   34.1%;  Pred. No. 7.2e-17;
  Matches   45;  Conservative   20;  Mismatches   63;  Indels    4;  Gaps    1;

Qy       1 STAPTRSKTP----AQGLARKLHFSTAPPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHAR 56
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Db     127 AVGPPRPRAPPGANAVASGRPLAFSAAPKTPKAPWCGPTHAYNRTIFCEAVALVAAEYAR 186

Qy      57 MAAVQLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQDVDAATATR 116
             ||  :||   |:::| |: :|    ||: ||||  ||  ||:::     :     : :
Db     187 QAAASVWDSDPPKSNERLDRMLKSAAIRILVCEGSGLLAAANDILAARAQRPAARGSTSG 246

Qy     117 GRSAASRPTERP 128
           | |       ||
Db     247 GESRLRGERARP 258


RESULT 9
US-09-213-343-2
; Sequence 2, Application US/09213343
; Patent No. 6316252
; GENERAL INFORMATION:
;  APPLICANT: Harms, Jerome S.
;  APPLICANT: Splitter, Gary A.
;  TITLE OF INVENTION: Biotherapeutic Delivery System
;  FILE REFERENCE: 960296.95564
;  CURRENT APPLICATION NUMBER: US/09/213,343
;  CURRENT FILING DATE: 1998-12-17
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 258
;   TYPE: PRT
;   ORGANISM: Bovine herpesvirus 1
US-09-213-343-2

  Query Match             28.5%;  Score 210;  DB 4;  Length 258;
  Best Local Similarity   34.1%;  Pred. No. 7.2e-17;
  Matches   45;  Conservative   20;  Mismatches   63;  Indels    4;  Gaps    1;

Qy       1 STAPTRSKTP----AQGLARKLHFSTAPPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHAR 56
           :  | | : |     |    | | || ||  | |||      :|: :|| ||  :|| :||
Db     127 AVGPPRPRAPPGANAVASGRPLAFSAAPKTPKAPWCGPTHAYNRTIFCEAVALVAAEYAR 186

Qy      57 MAAVQLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQDVDAATATR 116
             ||  :||   |:::| |: :|    ||: ||||  ||  ||:::     :     : :
Db     187 QAAASVWDSDPPKSNERLDRMLKSAAIRILVCEGSGLLAAANDILAARAQRPAARGSTSG 246

Qy     117 GRSAASRPTERP 128
           | |       ||
Db     247 GESRLRGERARP 258


RESULT 10
US-08-303-861-20
; Sequence 20, Application US/08303861
; Patent No. 6086902
; GENERAL INFORMATION:
;   APPLICANT:  ZAMB, TIMOTHY
;   APPLICANT:  LIANG, XIAOPING
;   APPLICANT:  BABIUK, LORNE A.
;   TITLE OF INVENTION:  RECOMBINANT BOVINE HERPESVIRUS TYPE I
;   TITLE OF INVENTION:  VACCINES
;   NUMBER OF SEQUENCES:  21
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  MORRISON & FOERSTER
;     STREET:  755 Page Mill Road
;     CITY:  Palo Alto
;     STATE:  California
;     COUNTRY:  USA
;     ZIP:  94304-1018
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/303,861
;     FILING DATE:  09-SEP-1994
;     CLASSIFICATION:  435
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  PARK, FREDDIE K.
;     REGISTRATION NUMBER:  35,636
;     REFERENCE/DOCKET NUMBER:  29310-20020.20
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (415) 813-5600
;     TELEFAX:  (415) 494-0792
;     TELEX:  706141
;  INFORMATION FOR SEQ ID NO:  20:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  302 amino acids
;     TYPE:  amino acid
;     STRANDEDNESS:  single
;     TOPOLOGY:  linear
US-08-303-861-20

  Query Match             27.8%;  Score 205;  DB 3;  Length 302;
  Best Local Similarity   34.8%;  Pred. No. 3.5e-16;
  Matches   56;  Conservative   18;  Mismatches   59;  Indels   28;  Gaps    3;

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           :| |:   |  :|  | : |||||    : |     :|||||| || |:||| |: ||
Db     139 SPKRAPPGAGAIASGRPISFSTAPKTATSSWCGPTPSYNKRVFCEAVRRVAAMQAQKAAE 198

Qy      61 QLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANE---------------------- 99
             |: : || : :|: ||    ||:|| || ||:| |||
Db     199 AAWNSNPPRNNAELDRLLTGAVIRITVHEGLNLIQAANEADLGEGASVSKRGHNRKTGDL 258

Qy     100 ---LVNPDVVQDVDAATATRGRSAASRPTERPRAPARSASR 137
               : |  :   |    :        | | | |  ||||||
Db     259 QGGMGNEPMYAQVRKPKSRTDTQTTGRITNRSR--ARSASR 297


RESULT 11
US-09-347-504-14
; Sequence 14, Application US/09347504
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OM protein - protein search, using sw model

Run on: May 21, 2003, 17:13:44 ; Search time 73.2162 Seconds
(without alignments)
547.808 Million cell updates/sec

Title: US-09-522-278B-12
Perfect score: 1561
Sequence: 1 MTSRRSVKSGPREVPRDEYE.....PTERPRAPARSASRPRRPVE 301

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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11: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:*
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13: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*
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21: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1561	100.0	301	20	AAY42292	Herpes simplex vir
2	1561	100.0	301	20	AAY27404	HSV-1 tegument pro
3	1561	100.0	301	22	AAB86329	VP22 protein fragm
4	1561	100.0	301	22	AAG64275	Herpes simplex vir
5	1561	100.0	667	22	AAE05266	VP22-Cre fusion pr
6	1561	100.0	747	22	AAE05267	VP22-Flpe fusion p
7	1557	99.7	418	23	AAU77235	PcDNA3-VP22/E7 fus
8	1557	99.7	683	22	AAE05273	VP22CreStrepTag fu
9	1554	99.6	301	20	AAW95099	HIV-1 VP22 polypep
10	1554	99.6	301	21	AAY79877	HSV-1 VP22 peptide
11	1554	99.6	301	22	AAB60910	HSV-1 VP22 protein
12	1554	99.6	301	23	ABB05524	HSV-1 VP22 protein
13	1553	99.5	301	19	AAW47194	Herpes simplex vir
14	1553	99.5	301	21	AAY83261	HSV-1 V22 cellular
15	1520	97.4	297	21	AAY96574	HSV-1 VP22 polypep
16	1392	89.2	267	22	AAB86330	VP22 protein fragm
17	1203.5	77.1	246	21	AAY78333	Herpes simplex vir
18	1203.5	77.1	246	23	AAE23170	Herpes simplex vir
19	1014.5	65.0	306	20	AAW67755	HSV-2 VP22 protein
20	1006.5	64.5	302	19	AAW72214	HSV-2 strain SB5 C
21	738	47.3	539	22	AAE05270	Delta VP22Cre-Stre
22	573	36.7	144	19	AAW47195	Herpes simplex vir
23	492	31.5	117	19	AAW72068	HSV-2 strain SB5 C
24	323	20.7	131	19	AAW72069	HSV-2 strain SB5 C
25	277	17.7	257	15	AAR63461	Deduced AA sequenc
26	271.5	17.4	258	21	AAB07662	Amino acid sequenc
27	271.5	17.4	258	23	AAU11367	Bovine herpesvirus
28	210	13.5	249	23	AAU77236	Marek's disease vi
29	205	13.1	249	16	AAR65493	Marek's disease vi
30	179	11.5	37	20	AAW95100	HIV-1 VP22 polypep
31	179	11.5	37	21	AAY96575	HSV-1 VP22 polypep
32	179	11.5	37	21	AAY83262	HSV-1 V22 C-termin
33	179	11.5	37	21	AAY79878	HSV-1 VP22 C-termi
34	179	11.5	37	22	AAB60911	HSV-1 VP22 C-termi
35	179	11.5	37	23	ABB05525	HSV-1 VP22 protein
36	172.5	11.1	139	18	AAW23003	Canine herpesvirus
37	172.5	11.1	139	19	AAW72663	Canine herpes viru
38	172.5	11.1	139	22	AAB51320	Canine herpes viru
39	169	10.8	34	23	AAM48195	Herpes simplex vir
40	168.5	10.8	388	23	ABG60300	Lymphona associate
41	168.5	10.8	388	23	ABB09271	G protein-coupled
42	168.5	10.8	451	22	AAU68528	Human novel cytoki
43	166	10.6	34	22	AAE12206	Membrane transport
44	164	10.5	34	23	AAU78347	Herpes simplex-1 v
45	164	10.5	35	23	AAU78354	Herpes simplex-1 v

ALIGNMENTS

RESULT 1
AAY42292
ID AAY42292 standard; Protein; 301 AA.
XX
AC AAY42292;
XX
DT 06-DEC-1999 (first entry)
XX
DE Herpes simplex virus type 1 (HSV-1) VP22 tegument protein.
XX
KW Cytochrome; targetting; localisation; cancer; tumour; prodrug; reduction;
KW nucleus.
XX
OS Herpes simplex virus type 1.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 251..267
FT /note= "Corresponding DNA sequence appears to be absent"
XX
PN WO9945127-A2.
XX
PD 10-SEP-1999.
XX
PF 05-MAR-1999; 99WO-GB00674.
XX
PR 06-MAR-1998; 98GB-0004841.
PR 19-AUG-1998; 98GB-0018103.
PR 29-JAN-1999; 99GB-0002081.
XX
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI Stratford IJ, Patterson AV, Kingsman SM, Kan O, Griffiths L;

PI Mitrophanous K;
XX
DR WPI; 1999-551046/46.
DR N-PSDB; AAZ19784.
XX
PT New prodrug activating agent targeted to selected cells or tissues,
PT particularly hypoxic cells, for treating e.g. tumors -
XX
PS Example 7; Fig 3; 187pp; English.
XX
CC This sequence represents a Herpes simplex virus type 1 (HSV-1)
CC VP22 tegument protein, which is involved in transcellular
CC localisation. VP22 can be fused to cytochrome P450 reductase (P450R)
CC derivatives such as anchorless P450R (AAY42287) or FN fragment
CC (AAY42288). This enables the fusion protein to be delivered to
CC neighbouring cells where it is then transported to the nucleus. Many
CC drugs' sites of action are in the nucleus, rather than the cytoplasm,
CC where P450R normally functions. P450R or its derivatives can be used to
CC activate prodrugs to their active form via reduction. Administration of a
CC prodrug is useful where the active drug may be metabolised before it
CC reaches its site of action or where the active drug is cytotoxic, e.g.,
CC anticancer drugs. Targetted delivery of such prodrug activators allows a
CC reduction in dose of the prodrug, and thus of systemic side-effects.
CC P450R derivative fusion proteins, or vectors that express them, are
CC specifically used to treat tumours, inflammation, atherosclerosis and
CC muscular dystrophy, but may also be used to treat many other conditions,
CC e.g., cerebral malaria, rheumatoid arthritis, or conditions associated
CC with hypoxia, ischaemia or hypoglycemia, or to deliver antibiotics,
CC antiviral agents, analgesics, anaesthetics, anti-inflammatories,
CC antineoplastic agents and diagnostic agents.
XX
SQ Sequence 301 AA;

Query Match 100.0%; Score 1561; DB 20; Length 301;
Best Local Similarity 100.0%; Pred. No. 6.4e-122;
Matches 301; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTSRRSVKSGPREVPRDEYEDLYYTPSSGMASPDSPPDTSRRGALQTRSRQRGEVRFVQY 60
Db 1 MTSRRSVKSGPREVPRDEYEDLYYTPSSGMASPDSPPDTSRRGALQTRSRQRGEVRFVQY 60

Qy 61 DESDYALYGGSSSEDDEHPEVPRTRRPVSGAVLSGPGPARAPPPPAGSGGAGRTPTTAPR 120
Db 61 DESDYALYGGSSSEDDEHPEVPRTRRPVSGAVLSGPGPARAPPPPAGSGGAGRTPTTAPR 120

Qy 121 APRTQRVATKAPAAPAAETTRGRKSAQPESAALPDAPASTAPTRSKTPAQGLARKLHFST 180
Db 121 APRTQRVATKAPAAPAAETTRGRKSAQPESAALPDAPASTAPTRSKTPAQGLARKLHFST 180

Qy 181 APPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAVQLWDMSRPRTDEDLNELLGITT 240
Db 181 APPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAVQLWDMSRPRTDEDLNELLGITT 240

Qy 241 IRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSAASRPTERPRAPARSASRPRRPV 300
Db 241 IRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSAASRPTERPRAPARSASRPRRPV 300

Qy 301 E 301
Db 301 E 301

RESULT 2
AAY27404
ID AAY27404 standard; Protein; 301 AA.
XX
AC AAY27404;
XX
DT 23-NOV-1999 (first entry)
XX
DE HSV-1 tegument protein VP22.
XX
KW Prodrug; localization domain; tumor-selective antibody; cytochrome P450;
KW prodrug activating domain; modified hematopoietic stem cell; MHSC; tumor;
KW inflammation; atherosclerosis; muscular dystrophy; cerebral malaria;
KW rheumatoid arthritis; hypoxia; ischemia; hypoglycemia; HSV; VP22;
KW tegument protein.
XX
OS Herpes simplex virus type 1.
XX
FH Key Location/Qualifiers
FT Region 251..267
FT /note= "the corresponding DNA sequence for this region
FT is possibly missing; there are only 4 nucleotide
FT basepairs indicated as encoding for this entire
FT region"
XX
PN WO9945126-A2.
XX
PD 10-SEP-1999.
XX
PF 05-MAR-1999; 99WO-GB00672.
XX
PR 06-MAR-1998; 98GB-0004841.
PR 19-AUG-1998; 98GB-0018103.
PR 29-JAN-1999; 99GB-0002081.
XX
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI Stratford IJ, Patterson AV, Kingsman SM, Kan O, Griffiths L;
PI Mitrophanous K;
XX
DR WPI; 1999-540852/45.
DR N-PSDB; AAZ07807.
XX
PT New prodrug activating agent targeted to selected cells or tissues,
PT particularly hypoxic cells, for treating e.g. tumors or inflammation -
XX
PS Example 7; Fig 3D; 149pp; English.
XX
CC The invention provides a new prodrug activating agent that comprises: (i)
CC a localization domain (LD; other than a tumor-selective antibody) and a
CC prodrug activating domain (PAD); (ii) at least one nucleic acid encoding
CC a cytochrome P450 and under control of at least one constitutive or
CC inducible expression control sequence or (iii) a modified hematopoietic
CC stem cell (MHSC) containing at least one nucleic acid encoding a PAD and
CC under control of elements as in (ii). The prodrug activating agent or
CC vectors that express them, are specifically used to treat tumors,
CC inflammation, atherosclerosis and muscular dystrophy, but may also be
CC used to treat many other conditions, e.g. cerebral malaria, rheumatoid
CC arthritis, or conditions associated with hypoxia, hypoglycemia or
CC ischemia, or to deliver antibiotics, antiviral agents, analgesics,
CC anesthetics, anti-inflammatories, antineoplastic agents and diagnostic
CC agents. LD optimize activity of PAD, e.g. by delivering it to selected
CC locations or by delivering it to neighboring cells (bystander effect),
CC and allow a reduction in dose of prodrug, and thus of systemic side-
CC effects. Nucleic acids encoding the agent may be expressed selectively
CC in hypoxic cells. The present sequence represents the HSV-1 tegument
CC protein VP22. This is used in the construction of a fusion protien
CC comprising VP22 and a human P450 reductase derivative alP450R.
XX
SQ Sequence 301 AA;

Query Match 100.0%; Score 1561; DB 20; Length 301;
Best Local Similarity 100.0%; Pred. No. 6.4e-122;
Matches 301; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTSRRSVKSGPREVPRDEYEDLYYTPSSGMASPDSPPDTSRRGALQTRSRQRGEVRFVQY 60
Db 1 MTSRRSVKSGPREVPRDEYEDLYYTPSSGMASPDSPPDTSRRGALQTRSRQRGEVRFVQY 60

Qy 61 DESDYALYGGSSSEDDEHPEVPRTRRPVSGAVLSGPGPARAPPPPAGSGGAGRTPTTAPR 120
Db 61 DESDYALYGGSSSEDDEHPEVPRTRRPVSGAVLSGPGPARAPPPPAGSGGAGRTPTTAPR 120

Qy 121 APRTQRVATKAPAAPAAETTRGRKSAQPESAALPDAPASTAPTRSKTPAQGLARKLHFST 180

```
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Db    121 APRTQRVATKAPAAPAAETTRGRKSAQPESAALPDAPASTAPTRSKTPAQGLARKLHFST 180

Qy    181 APPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAVQLWDMSRPRTDEDLNELLGITT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 APPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAVQLWDMSRPRTDEDLNELLGITT 240

Qy    241 IRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSAASRPTERPRAPARSASRPRRPV 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 IRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSAASRPTERPRAPARSASRPRRPV 300

Qy    301 E 301
          |
Db    301 E 301


RESULT 3
AAB86329
ID   AAB86329 standard; Protein; 301 AA.
XX
AC   AAB86329;
XX
DT   18-SEP-2001  (first entry)
XX
DE   VP22 protein fragment.
XX
KW   Fusion protein; VP22; E7; cell import signal; cell export signal;
KW   antigen; immunization; infection-induced auto-immune disease;
KW   tumor disease.
XX
OS   Unidentified.
XX
PN   WO200151516-A2.
XX
PD   19-JUL-2001.
XX
PF   15-JAN-2001; 2001WO-DE00134.
XX
PR   13-JAN-2000; 2000DE-1001230.
XX
PA   (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
PI   Mueller M,  Michel N,  Osen W,  Gissmann L,  Zentgraf H;
XX
DR   WPI; 2001-442135/47.
XX
PT   Identifying an immunization agent comprising cell import and/or
PT   export signal sequences and an antigen for immunizing against
PT   infection-induced auto-immune and tumor disease -
XX
PS   Disclosure; Fig 4; 23pp; German.
XX
CC   This invention describes a fusion protein comprising cell import and/or
CC   export signal sequences and an antigen which is suitable for immunizing
CC   an individual against a disease, together with a DNA that codes for said
CC   protein. The invention also relates to the use of the protein (II) and
CC   its encoding DNA (I) for immunizing an individual against diseases, in
CC   particular against infection-induced auto-immune and tumor disease. This
CC   sequence represents the VP22 protein fragment used in the construction of
CC   the fusion construct VP22-E7.
XX
SQ   Sequence   301 AA;

  Query Match           100.0%;  Score 1561;  DB 22;  Length 301;
  Best Local Similarity  100.0%;  Pred. No. 6.4e-122;
  Matches  301;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db      1 MTSRRSVKSGPREVPRDEYEDLYYTPSSGMASPDSPPDTSRRGALQTRSRQRGEVRFVQY 60

Qy     61 DESDYALYGGSSSEDDEHPEVPRTRRPVSGAVLSGPGPARAPPPPAGSGGAGRTPTTAPR 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 DESDYALYGGSSSEDDEHPEVPRTRRPVSGAVLSGPGPARAPPPPAGSGGAGRTPTTAPR 120

Qy    121 APRTQRVATKAPAAPAAETTRGRKSAQPESAALPDAPASTAPTRSKTPAQGLARKLHFST 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 APRTQRVATKAPAAPAAETTRGRKSAQPESAALPDAPASTAPTRSKTPAQGLARKLHFST 180

Qy    181 APPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAVQLWDMSRPRTDEDLNELLGITT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 APPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAVQLWDMSRPRTDEDLNELLGITT 240

Qy    241 IRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSAASRPTERPRAPARSASRPRRPV 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 IRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSAASRPTERPRAPARSASRPRRPV 300

Qy    301 E 301
          |
Db    301 E 301


RESULT 4
AAG64275
ID   AAG64275 standard; protein; 301 AA.
XX
AC   AAG64275;
XX
DT   21-SEP-2001  (first entry)
XX
DE   Herpes simplex viral protein: SEQ ID 26.
XX
KW   BH4 domain; cardiant; anti-HIV; neuroprotective; hepatotropic; Bcl-2;
KW   antidiabetic; apoptosis inhibitor; cellular uptake; anti-apoptosis;
KW   ischaemic disease; myocardial infarct; AIDS; neurodegenerative diseases;
KW   infective multiple failure; fulminant hepatitis; diabetes.
XX
OS   Herpes simplex virus type 1.
XX
PN   WO200148014-A1.
XX
PD   05-JUL-2001.
XX
PF   26-DEC-2000; 2000WO-JP09274.
XX
PR   27-DEC-1999;  99JP-0371449.
XX
PA   (SHIO ) SHIONOGI & CO LTD.
XX
PI   Shimizu S,  Tsujimoto Y;
XX
DR   WPI; 2001-418246/44.
XX
PT   BH4-fused polypeptides with peptide sequences capable of exerting
PT   effect on enabling uptake into cells, applicable as effective apoptosis
PT   inhibitors, useful in preventives or remedies for ischemic diseases
PT   e.g. myocardial infarct -
XX
PS   Claim 5; Page 74-6; 84pp; Japanese.
XX
CC   The present invention relates to BH4-fused polypeptides. The BH4-fused
CC   polypeptide have a sequence capable of affecting cellular uptake and also
CC   a BH4 domain sequence from an anti-apoptosis Bcl-2 family protein. The
CC   BH4-fused polypeptides are useful as effective apoptosis inhibitors, and
CC   are useful in preventives or remedies for ischaemic diseases e.g.
CC   myocardial infarct, AIDS, neurodegenerative diseases, infective multiple
CC   failure, fulminant hepatitis and diabetes. The present peptide was used
CC   in the present invention.
XX
SQ   Sequence   301 AA;

  Query Match           100.0%;  Score 1561;  DB 22;  Length 301;
  Best Local Similarity  100.0%;  Pred. No. 6.4e-122;
  Matches  301;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 MTSRRSVKSGPREVPRDEYEDLYYTPSSGMASPDSPPDTSRRGALQTRSRQRGEVRFVQY 60
```

```
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MTSRRSVKSGPREVPRDEYEDLYYTPSSGMASPDSPPDTSRRGALQTRSRQRGEVRFVQY 60

Qy     61 DESDYALYGGSSSEDDEHPEVPRTRRPVSGAVLSGPGPARAPPPPAGSGGAGRTPTTAPR 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 DESDYALYGGSSSEDDEHPEVPRTRRPVSGAVLSGPGPARAPPPPAGSGGAGRTPTTAPR 120

Qy    121 APRTQRVATKAPAAPAAETTRGRKSAQPESAALPDAPASTAPTRSKTPAQGLARKLHFST 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 APRTQRVATKAPAAPAAETTRGRKSAQPESAALPDAPASTAPTRSKTPAQGLARKLHFST 180

Qy    181 APPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAVQLWDMSRPRTDEDLNELLGITT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 APPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAVQLWDMSRPRTDEDLNELLGITT 240

Qy    241 IRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSAASRPTERPRAPARSASRPRRPV 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 IRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSAASRPTERPRAPARSASRPRRPV 300

Qy    301 E 301
          |
Db    301 E 301
```

RESULT 5
AAE05266
ID AAE05266 standard; Protein; 667 AA.
XX
AC AAE05266;
XX
DT 12-SEP-2001 (first entry)
XX
DE VP22-Cre fusion protein.
XX
KW DNA recombinase domain; protein transduction domain; PTD;
KW gene alteration; VP22-Cre fusion protein; Human immunodeficiency virus;
KW HIV; Human spumaretrovirus; HSV.
XX
OS Chimeric - Human spumaretrovirus.
OS Chimeric - Unidentified.
XX
PN WO200149832-A2.
XX
PD 12-JUL-2001.
XX
PF 05-JAN-2001; 2001WO-EP00060.
XX
PR 07-JAN-2000; 2000EP-0100351.
PR 10-NOV-2000; 2000EP-0124595.
XX
PA (ARTE-) ARTEMIS PHARM GMBH.
XX
PI Schwenk F;
XX
DR WPI; 2001-441873/47.
DR N-PSDB; AAD09259.
XX
PT Using site-specific DNA recombinase domain/protein transduction domain
PT fusion proteins for inducing target gene alterations in organisms or
PT cell cultures -
XX
PS Claim 12; Page 35-37; 85pp; English.
XX
CC The present invention relates to use of fusion proteins comprising
CC a site-specific DNA recombinase domain e.g. Cre and a protein
CC transduction domain (PTD) e.g. the Human immunodeficiency virus
CC (HIV) derived TAT peptide, for preparing an agent for inducing
CC target gene alterations in a living organism or cell culture. The
CC present invention also provides a method for inducing gene
CC alterations in living organisms using the fusion proteins of the
CC invention. The present sequence is VP22-Cre fusion protein. The
CC VP22 sequence is from Human spumaretrovirus (HSV).
XX

SQ Sequence 667 AA;

Query Match 100.0%; Score 1561; DB 22; Length 667;
Best Local Similarity 100.0%; Pred. No. 1.7e-121;
Matches 301; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MTSRRSVKSGPREVPRDEYEDLYYTPSSGMASPDSPPDTSRRGALQTRSRQRGEVRFVQY 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MTSRRSVKSGPREVPRDEYEDLYYTPSSGMASPDSPPDTSRRGALQTRSRQRGEVRFVQY 60

Qy     61 DESDYALYGGSSSEDDEHPEVPRTRRPVSGAVLSGPGPARAPPPPAGSGGAGRTPTTAPR 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 DESDYALYGGSSSEDDEHPEVPRTRRPVSGAVLSGPGPARAPPPPAGSGGAGRTPTTAPR 120

Qy    121 APRTQRVATKAPAAPAAETTRGRKSAQPESAALPDAPASTAPTRSKTPAQGLARKLHFST 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 APRTQRVATKAPAAPAAETTRGRKSAQPESAALPDAPASTAPTRSKTPAQGLARKLHFST 180

Qy    181 APPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAVQLWDMSRPRTDEDLNELLGITT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 APPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAVQLWDMSRPRTDEDLNELLGITT 240

Qy    241 IRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSAASRPTERPRAPARSASRPRRPV 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 IRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSAASRPTERPRAPARSASRPRRPV 300

Qy    301 E 301
          |
Db    301 E 301
```

RESULT 6
AAE05267
ID AAE05267 standard; Protein; 747 AA.
XX
AC AAE05267;
XX
DT 12-SEP-2001 (first entry)
XX
DE VP22-Flpe fusion protein.
XX
KW DNA recombinase domain; protein transduction domain; PTD;
KW gene alteration; VP22-Flpe fusion protein; Human immunodeficiency virus;
KW HIV; Human spumaretrovirus; HSV.
XX
OS Chimeric - Human spumaretrovirus.
OS Chimeric - Unidentified.
XX
PN WO200149832-A2.
XX
PD 12-JUL-2001.
XX
PF 05-JAN-2001; 2001WO-EP00060.
XX
PR 07-JAN-2000; 2000EP-0100351.
PR 10-NOV-2000; 2000EP-0124595.
XX
PA (ARTE-) ARTEMIS PHARM GMBH.
XX
PI Schwenk F;
XX
DR WPI; 2001-441873/47.
DR N-PSDB; AAD09260.
XX
PT Using site-specific DNA recombinase domain/protein transduction domain
PT fusion proteins for inducing target gene alterations in organisms or
PT cell cultures -
XX
PS Claim 12; Page 40-43; 85pp; English.
XX
CC The present invention relates to use of fusion proteins comprising
CC a site-specific DNA recombinase domain e.g. Cre and a protein
CC transduction domain (PTD) e.g. the Human immunodeficiency virus

```
CC   (HIV) derived TAT peptide, for preparing an agent for inducing
CC   target gene alterations in a living organism or cell culture. The
CC   present invention also provides a method for inducing gene
CC   alterations in living organisms using the fusion proteins of the
CC   invention. The present sequence is VP22-Flpe fusion protein. The
CC   VP22 sequence is from Human spumaretrovirus (HSV).
XX
SQ   Sequence   747 AA;

  Query Match             100.0%;  Score 1561;  DB 22;  Length 747;
  Best Local Similarity   100.0%;  Pred. No. 2e-121;
  Matches  301;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MTSRRSVKSGPREVPRDEYEDLYYTPSSGMASPDSPPDTSRRGALQTRSRQRGEVRFVQY 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MTSRRSVKSGPREVPRDEYEDLYYTPSSGMASPDSPPDTSRRGALQTRSRQRGEVRFVQY 60

Qy      61 DESDYALYGGSSSEDDEHPEVPRTRRPVSGAVLSGPGPARAPPPPAGSGGAGRTPTTAPR 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 DESDYALYGGSSSEDDEHPEVPRTRRPVSGAVLSGPGPARAPPPPAGSGGAGRTPTTAPR 120

Qy     121 APRTQRVATKAPAAPAAETTRGRKSAQPESAALPDAPASTAPTRSKTPAQGLARKLHFST 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 APRTQRVATKAPAAPAAETTRGRKSAQPESAALPDAPASTAPTRSKTPAQGLARKLHFST 180

Qy     181 APPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAVQLWDMSRPRTDEDLNELLGITT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 APPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAVQLWDMSRPRTDEDLNELLGITT 240

Qy     241 IRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSAASRPTERPRAPARSASRPRRPV 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 IRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSAASRPTERPRAPARSASRPRRPV 300

Qy     301 E 301
           |
Db     301 E 301


RESULT 7
AAU77235
ID   AAU77235 standard; Protein; 418 AA.
XX
AC   AAU77235;
XX
DT   05-JUN-2002  (first entry)
XX
DE   PcDNA3-VP22/E7 fusion protein sequence.
XX
KW   Virucide; cytostatic; vaccine; intercellular transport; antigenic;
KW   immune response; cytotoxic T lymphocyte; tumour; cancer; pcDNA3-VP22/E7;
KW   chronic viral infection; veterinary herpesvirus infection; pseudorabies;
KW   equine herpesvirus; bovine herpesvirus; Marek's disease virus; chicken;
KW   fowl; animal retroviral disease; rabies; fusion protein.
XX
OS   Chimeric - herpes simplex virus type 1.
OS   Chimeric - human papilloma virus type 16.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Protein         1..301
FT                   /note= "VP22 transport polypeptide from herpes simplex
FT                         virus type 1, specifically claimed in claim 10"
FT   Region          302..307
FT                   /note= "Linker sequence"
FT   Protein         308..403
FT                   /note= "Represents 96 of the 98 residues of E7 from
FT                         human papilloma virus type 16"
FT   Region          404..418
FT                   /note= "Vector sequence"
XX
PN   WO200209645-A2.
XX
PD   07-FEB-2002.
XX
PF   01-AUG-2001; 2001WO-US23966.
XX
PR   01-AUG-2000; 2000US-222185P.
PR   15-FEB-2001; 2001US-268575P.
PR   04-APR-2001; 2001US-281004P.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Wu T,  Hung C;
XX
DR   WPI; 2002-257367/30.
DR   N-PSDB; ABK11810.
XX
PT   New nucleic acids encoding fusion polypeptide comprising intercellular
PT   transport polypeptide linked to antigenic polypeptide, useful as
PT   therapeutic vaccine for cancer and major chronic viral infections -
XX
PS   Disclosure; Fig 7; 102pp; English.
XX
CC   The present invention relates to a new nucleic acid molecule that
CC   encodes a fusion polypeptide. The fusion protein comprises a first
CC   polypeptide comprising at least one intercellular transport polypeptide
CC   and a second polypeptide comprising at least one antigenic polypeptide
CC   or peptide. The invention also describes an optional linker peptide
CC   linking the first and second polypeptide. The nucleic acid is useful as
CC   a vaccine for enhancing immune responses, primarily cytotoxic T
CC   lymphocyte responses to specific antigens such as tumour or viral
CC   antigens. The compositions comprising the nucleic acids are especially
CC   useful as a therapeutic vaccine for cancer and for major chronic viral
CC   infections, as well as in the treatment of veterinary herpesvirus
CC   infections, including equine or bovine herpesvirus, Marek's disease virus
CC   in chickens and other fowls, animal retroviral diseases, pseudorabies
CC   and rabies. The present amino acid sequence represents the pcDNA3-VP22/E7
CC   fusion protein of the invention.
XX
SQ   Sequence   418 AA;

  Query Match             99.7%;  Score 1557;  DB 23;  Length 418;
  Best Local Similarity   99.7%;  Pred. No. 2.1e-121;
  Matches  300;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MTSRRSVKSGPREVPRDEYEDLYYTPSSGMASPDSPPDTSRRGALQTRSRQRGEVRFVQY 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MTSRRSVKSGPREVPRDEYEDLYYTPSSGMASPDSPPDTSRRGALQTRSRQRGEVRFVQY 60

Qy      61 DESDYALYGGSSSEDDEHPEVPRTRRPVSGAVLSGPGPARAPPPPAGSGGAGRTPTTAPR 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 DESDYALYGGSSSEDDEHPEVPRTRRPVSGAVLSGPGPARAPPPPAGSGGAGRTPTTAPR 120

Qy     121 APRTQRVATKAPAAPAAETTRGRKSAQPESAALPDAPASTAPTRSKTPAQGLARKLHFST 180
           ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 APRTQRVASKAPAAPAAETTRGRKSAQPESAALPDAPASTAPTRSKTPAQGLARKLHFST 180

Qy     181 APPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAVQLWDMSRPRTDEDLNELLGITT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 APPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAVQLWDMSRPRTDEDLNELLGITT 240

Qy     241 IRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSAASRPTERPRAPARSASRPRRPV 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 IRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSAASRPTERPRAPARSASRPRRPV 300

Qy     301 E 301
           |
Db     301 E 301


RESULT 8
AAE05273
ID   AAE05273 standard; Protein; 683 AA.
XX
AC   AAE05273;
XX
```

```
DT   12-SEP-2001  (first entry)
XX
DE   VP22CreStrepTag fusion protein.
XX
KW   DNA recombinase domain; protein transduction domain; PTD;
KW   VP22CreStrepTag fusion protein; Human immunodeficiency virus; HIV;
KW   gene alteration; Human spumaretrovirus; HSV.
XX
OS   Chimeric - Human spumaretrovirus.
OS   Chimeric - Unidentified.
XX
PN   WO200149832-A2.
XX
PD   12-JUL-2001.
XX
PF   05-JAN-2001; 2001WO-EP00060.
XX
PR   07-JAN-2000; 2000EP-0100351.
PR   10-NOV-2000; 2000EP-0124595.
XX
PA   (ARTE-) ARTEMIS PHARM GMBH.
XX
PI   Schwenk F;
XX
DR   WPI; 2001-441873/47.
DR   N-PSDB; AAD09268.
XX
PT   Using site-specific DNA recombinase domain/protein transduction domain
PT   fusion proteins for inducing target gene alterations in organisms or
PT   cell cultures -
XX
PS   Disclosure; Page 58-60; 85pp; English.
XX
CC   The present invention relates to use of fusion proteins comprising
CC   a site-specific DNA recombinase domain e.g. Cre and a protein
CC   transduction domain (PTD) e.g. the Human immunodeficiency virus
CC   (HIV) derived TAT peptide, for preparing an agent for inducing
CC   target gene alterations in a living organism or cell culture. The
CC   present invention also provides a method for inducing gene
CC   alterations in living organisms using the fusion proteins of the
CC   invention. The present sequence is VP22CreStrepTag fusion protein.
CC   The VP22 sequence is from Human spumaretrovirus (HSV).
XX
SQ   Sequence   683 AA;

  Query Match             99.7%;  Score 1557;  DB 22;  Length 683;
  Best Local Similarity   99.7%;  Pred. No. 3.8e-121;
  Matches  300;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MTSRRSVKSGPREVPRDEYEDLYYTPSSGMASPDSPPDTSRRGALQTRSRQRGEVRFVQY 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MTSRRSVKSGPREVPRDEYEDLYYTPSSGMASPDSPPDTSRRGALQTRSRQRGEVRFVQY 60

Qy      61 DESDYALYGGSSSEDDEHPEVPRTRRPVSGAVLSGPGPARAPPPPAGSGGAGRTPTTAPR 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 DESDYALYGGSSSEDDEHPEVPRTRRPVSGAVLSGPGPARAPPPPAGSGGAGRTPTTAPR 120

Qy     121 APRTQRVATKAPAAPAAETTRGRKSAQPESAALPDAPASTAPTRSKTPAQGLARKLHFST 180
           ||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 APRTQRVASKAPAAPAAETTRGRKSAQPESAALPDAPASTAPTRSKTPAQGLARKLHFST 180

Qy     181 APPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAVQLWDMSRPRTDEDLNELLGITT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 APPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAVQLWDMSRPRTDEDLNELLGITT 240

Qy     241 IRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSAASRPTERPRAPARSASRPRRPV 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 IRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSAASRPTERPRAPARSASRPRRPV 300

Qy     301 E 301
           |
Db     301 E 301
```

```
RESULT 9
AAW95099
ID   AAW95099 standard; Protein; 301 AA.
XX
AC   AAW95099;
XX
DT   25-MAY-1999  (first entry)
XX
DE   HIV-1 VP22 polypeptide.
XX
KW   Cyclin-dependent kinase; CDK; CDK/cyclin complex; inhibitory; restenosis;
KW   CDK-binding motif; endothelialisation; fusion protein; therapeutic; acne;
KW   intracellular; transcellular; transcytosis; vascular wound; repair; hair;
KW   smooth muscle; cardiovascular; arteriosclerotic; fibrotic disorder;
KW   cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft;
KW   tumour; inflammation; neurodegeneration; periodontal; spermatogenesis;
KW   tachycardia; HIV-1.
XX
OS   Human immunodeficiency virus type 1.
XX
PN   WO9906540-A2.
XX
PD   11-FEB-1999.
XX
PF   29-JUL-1998;   98WO-US15759.
XX
PR   29-JUL-1997;   97US-0902572.
XX
PA   (MITO-) MITOTIX INC.
XX
PI   Beach DH,  Gyuris J,  Lamphere L;
XX
DR   WPI; 1999-153770/13.
DR   N-PSDB; AAX26227.
XX
PT   Fusion and chimaeric proteins including cyclin-dependent kinase
PT   binding motif - used for regulation of cell proliferation and
PT   differentiation, for treatment of, e.g. vascular injury, cancers,
PT   fibrosis and neurodegeneration
XX
PS   Example 2; Page 26-27; 88pp; English.
XX
CC   The invention relates to novel inhibitors of cyclin-dependent kinases
CC   (CDKs), particularly CDK/cyclin complexes. It provides a recombinant
CC   transfection system (A) that comprises: (i) first gene construct
CC   comprising a sequence encoding an inhibitory polypeptide containing at
CC   least one CDK-binding motif for binding and inhibiting activity of a
CC   CDK, linked to a transcription regulator functional in eukaryotic cells;
CC   (ii) second gene construct comprising a sequence encoding a polypeptide
CC   that promotes endothelialisation, and (iii) a gene delivery composition
CC   for delivering the GCs to a cell for transfection.  Also provided are
CC   nucleic acids encoding a fusion protein (FP) containing: (i) a
CC   therapeutic polypeptide sequence (TP) from an intracellular protein that
CC   alters a cellular process when FP enters the cell, and (ii) a
CC   transcellular polypeptide sequence (TCP) that promotes transcytosis of
CC   FP. The FP consists of at least one CDK-binding motif and a TCP. See
CC   AAX26220 for detailed uses of the recombinant transfection system.  The
CC   CKI polypeptides are engineered to include any of the peptides shown in
CC   AAW95097-100 encoded by the DNA sequences AAX26225-228.
XX
SQ   Sequence   301 AA;

  Query Match             99.6%;  Score 1554;  DB 20;  Length 301;
  Best Local Similarity   99.7%;  Pred. No. 2.5e-121;
  Matches  300;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MTSRRSVKSGPREVPRDEYEDLYYTPSSGMASPDSPPDTSRRGALQTRSRQRGEVRFVQY 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MTSRRSVKSGPREVPRDEYEDLYYTPSSGMASPDSPPDTSRRGALQTRSRQRGEVRFVQY 60

Qy      61 DESDYALYGGSSSEDDEHPEVPRTRRPVSGAVLSGPGPARAPPPPAGSGGAGRTPTTAPR 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db     61 DESDYALYGGSSSEDDEHPEVPRTRRPVSGAVLSGPGPARAPPPPAGSGGAGRTPTTAPR 120

Qy    121 APRTQRVATKAPAAPAAETTRGRKSAQPESAALPDAPASTAPTRSKTPAQGLARKLHFST 180
          |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 APRTGRVATKAPAAPAAETTRGRKSAQPESAALPDAPASTAPTRSKTPAQGLARKLHFST 180

Qy    181 APPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAVQLWDMSRPRTDEDLNELLGITT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 APPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAVQLWDMSRPRTDEDLNELLGITT 240

Qy    241 IRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSAASRPTERPRAPARSASRPRRPV 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 IRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSAASRPTERPRAPARSASRPRRPV 300

Qy    301 E 301
          |
Db    301 E 301


RESULT 10
AAY79877
ID   AAY79877 standard; Peptide; 301 AA.
XX
AC   AAY79877;
XX
DT   10-MAY-2000  (first entry)
XX
DE   HSV-1 VP22 peptide.
XX
KW   Papillomavirus; PV; infection; cell proliferation; E2; peptidomimetic;
KW   E1; antiviral; virucide; cytostatic; antiproliferative; dermatological;
KW   preneoplastic lesion; neoplastic lesion; cutaneous lesion; wart;
KW   epidermodysplasia verruciformis; anorectal carcinoma.
XX
OS   Herpes simplex virus type 1.
XX
PN   WO200001720-A2.
XX
PD   13-JAN-2000.
XX
PF   02-JUL-1999;   99WO-US15144.
XX
PR   02-JUL-1998;   98US-0091661.
XX
PA   (HARD ) HARVARD COLLEGE.
XX
PI   Howley P,  Benson J,  Kasukawa H;
XX
DR   WPI; 2000-171001/15.
DR   N-PSDB; AAZ88468.
XX
PT   Use of papillomavirus E2 protein peptidomimetics for treating
PT   papillomavirus-infected cells and papillomavirus-induced conditions in
PT   mammals by inhibiting E1-E2 interaction -
XX
PS   Disclosure; Page 42; 110pp; English.
XX
CC   The present invention describes the use of a small organic compound (A)
CC   which competitively inhibits interaction of a papillomavirus (PV) E2
CC   protein with a PV E1 protein for treating a cell infected with PV or a
CC   mammal with a PV-induced condition. (A) has antiviral, virucide,
CC   cytostatic, antiproliferative and dermatological activities. Methods
CC   from the present invention can be used to treat PV-induced conditions
CC   including growth of PV preneoplastic and neoplastic lesions, cutaneous
CC   lesions chosen from warts and other benign cutaneous lesions, plantar
CC   warts (verruca plantaris), common warts (verruca plana), Butcher's
CC   common warts, flat warts, genital warts (condyloma acuminatum) and
CC   epidermodysplasia verruciformis, laryngeal, oral, pharyngeal,
CC   oesophageal and other upper airway papilloma or vaginal, cervical,
CC   vulvar, penile and anorectal carcinoma. The E2 inhibitors may also be
CC   used to treat epithelial and internal fibropapillomas in animals.
CC   The present sequence represents a peptide sequence used in the
CC   exemplification of the present invention.
XX
SQ   Sequence   301 AA;

  Query Match             99.6%;  Score 1554;  DB 21;  Length 301;
  Best Local Similarity   99.7%;  Pred. No. 2.5e-121;
  Matches  300;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 MTSRRSVKSGPREVPRDEYEDLYYTPSSGMASPDSPPDTSRRGALQTRSRQRGEVRFVQY 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MTSRRSVKSGPREVPRDEYEDLYYTPSSGMASPDSPPDTSRRGALQTRSRQRGEVRFVQY 60

Qy     61 DESDYALYGGSSSEDDEHPEVPRTRRPVSGAVLSGPGPARAPPPPAGSGGAGRTPTTAPR 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 DESDYALYGGSSSEDDEHPEVPRTRRPVSGAVLSGPGPARAPPPPAGSGGAGRTPTTAPR 120

Qy    121 APRTQRVATKAPAAPAAETTRGRKSAQPESAALPDAPASTAPTRSKTPAQGLARKLHFST 180
          |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 APRTGRVATKAPAAPAAETTRGRKSAQPESAALPDAPASTAPTRSKTPAQGLARKLHFST 180

Qy    181 APPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAVQLWDMSRPRTDEDLNELLGITT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 APPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAVQLWDMSRPRTDEDLNELLGITT 240

Qy    241 IRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSAASRPTERPRAPARSASRPRRPV 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 IRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSAASRPTERPRAPARSASRPRRPV 300

Qy    301 E 301
          |
Db    301 E 301


RESULT 11
AAB60910
ID   AAB60910 standard; Protein; 301 AA.
XX
AC   AAB60910;
XX
DT   05-NOV-2001  (first entry)
XX
DE   HSV-1 VP22 protein.
XX
KW   Co-activator domain; P300/CBP KIX domain; erythrocythaemia; skin disease;
KW   polycythaemia; haemoglobinopathy; cell differentiation; ulcer; cancer;
KW   neurological condition; neurodegenerative disease; immune disease;
KW   diabetes.
XX
OS   Synthetic.
XX
PN   WO200118036-A2.
XX
PD   15-MAR-2001.
XX
PF   31-AUG-2000; 2000WO-US24010.
XX
PR   03-SEP-1999;   99US-0152402.
XX
PA   (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
PA   (JOSL-) JOSLIN DIABETES CENT INC.
XX
PI   Frangioni JV,  Cantley LC,  Montminy MR;
XX
DR   WPI; 2001-273380/28.
DR   N-PSDB; AAF58996.
XX
PT   Identifying co-activator domain specific transcriptional activators by
PT   contacting a target domain of a selected transcription factor with a
PT   peptide display library, where the identified binding peptides are
PT   useful for reducing hyperglycemia -
XX
PS   Disclosure; Page 78; 156pp; English.
XX
CC   The present invention describes a method of identifying the co-activator
```

```
CC   domain of specific synthetic activators, involving contacting the target
CC   domain of a selected transcription factor with a peptide display library,
CC   and identifying those sequences which bind to the target domain. In
CC   particular, those which bind to the KIX domain of P300/CBP are useful.
CC   The peptides can be used in the treatment of diseases related to aberrant
CC   KIX-dependent gene transcription, including erythrocythaemia,
CC   polycythaemia, haemoglobinopathies, to regulate cell differentiation, to
CC   treat neurological diseases, immunological diseases, diabetes, ulcers,
CC   skin diseases and cancer, and to aid wound healing. The present sequence
CC   is a protein described in the exemplification of the invention.
XX
SQ   Sequence   301 AA;

  Query Match             99.6%;  Score 1554;  DB 22;  Length 301;
  Best Local Similarity   99.7%;  Pred. No. 2.5e-121;
  Matches  300;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MTSRRSVKSGPREVPRDEYEDLYYTPSSGMASPDSPPDTSRRGALQTRSRQRGEVRFVQY 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MTSRRSVKSGPREVPRDEYEDLYYTPSSGMASPDSPPDTSRRGALQTRSRQRGEVRFVQY 60

Qy      61 DESDYALYGGSSSEDDEHPEVPRTRRPVSGAVLSGPGPARAPPPPAGSGGAGRTPTTAPR 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 DESDYALYGGSSSEDDEHPEVPRTRRPVSGAVLSGPGPARAPPPPAGSGGAGRTPTTAPR 120

Qy     121 APRTQRVATKAPAAPAAETTRGRKSAQPESAALPDAPASTAPTRSKTPAQGLARKLHFST 180
           |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 APRTGRVATKAPAAPAAETTRGRKSAQPESAALPDAPASTAPTRSKTPAQGLARKLHFST 180

Qy     181 APPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAVQLWDMSRPRTDEDLNELLGITT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 APPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAVQLWDMSRPRTDEDLNELLGITT 240

Qy     241 IRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSAASRPTERPRAPARSASRPRRPV 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 IRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSAASRPTERPRAPARSASRPRRPV 300

Qy     301 E 301
           |
Db     301 E 301


RESULT 12
ABB05524
ID   ABB05524 standard; Protein; 301 AA.
XX
AC   ABB05524;
XX
DT   22-APR-2002  (first entry)
XX
DE   HSV-1 VP22 protein.
XX
KW   Ubiquitin dependent proteolysis modulation; cdc4 phospho design motif;
KW   CDP motif; cytostatic; nootropic; antiproliferative; cell proliferation;
KW   growth; differentiation; cancer; neurodegenerative disorder;
KW   spinal degeneration.
XX
OS   Herpes simplex virus.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 125
FT                   /note= "encoded by CAG"
XX
PN   WO200183518-A2.
XX
PD   08-NOV-2001.
XX
PF   04-MAY-2001; 2001WO-CA00632.
XX
PR   04-MAY-2000; 2000US-202166P.
PR   24-JAN-2001; 2001US-263774P.
XX
PA   (MOUN ) MOUNT SINAI HOSPITAL.
XX
PI   Nash P,  Pawson T,  Tang X,  Tyers M;
XX
DR   WPI; 2002-164074/21.
DR   N-PSDB; ABA93386.
XX
PT   New Cdc4 Phospho Design motif that targets molecules for ubiquitin
PT   dependent proteolysis, is useful for the modulation of cell
PT   proliferation i.e. cancer treatment -
XX
PS   Disclosure; Page 30; 83pp; English.
XX
CC   The present invention describes a cdc4 phospho design (CPD) motif, (C),
CC   that targets molecules for ubiquitin dependent proteolysis. (C) have
CC   cytostatic, nootropic and antiproliferative activity. Also described is
CC   a method for the treatment of a disease or condition where affected
CC   cells have a defective protein, comprising administering (C) to promote
CC   degradation of the target protein in cells by ubiquitin dependent
CC   proteolysis. (C) can also be used for modulating the proliferation,
CC   growth and/or differentiation of cells. (C) can be used to modulate
CC   ubiquitin dependent proteolysis or cell proliferation, growth and or
CC   differentiation of cells. (C) is useful in the treatment of cancers and
CC   neurodegenerative disorders as well as spinal degeneration. The present
CC   sequence represents the HSV-1 VP22 protein which is given in the
CC   exemplification of the present invention.
XX
SQ   Sequence   301 AA;

  Query Match             99.6%;  Score 1554;  DB 23;  Length 301;
  Best Local Similarity   99.7%;  Pred. No. 2.5e-121;
  Matches  300;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MTSRRSVKSGPREVPRDEYEDLYYTPSSGMASPDSPPDTSRRGALQTRSRQRGEVRFVQY 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MTSRRSVKSGPREVPRDEYEDLYYTPSSGMASPDSPPDTSRRGALQTRSRQRGEVRFVQY 60

Qy      61 DESDYALYGGSSSEDDEHPEVPRTRRPVSGAVLSGPGPARAPPPPAGSGGAGRTPTTAPR 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 DESDYALYGGSSSEDDEHPEVPRTRRPVSGAVLSGPGPARAPPPPAGSGGAGRTPTTAPR 120

Qy     121 APRTQRVATKAPAAPAAETTRGRKSAQPESAALPDAPASTAPTRSKTPAQGLARKLHFST 180
           |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 APRTGRVATKAPAAPAAETTRGRKSAQPESAALPDAPASTAPTRSKTPAQGLARKLHFST 180

Qy     181 APPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAVQLWDMSRPRTDEDLNELLGITT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 APPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAVQLWDMSRPRTDEDLNELLGITT 240

Qy     241 IRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSAASRPTERPRAPARSASRPRRPV 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 IRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSAASRPTERPRAPARSASRPRRPV 300

Qy     301 E 301
           |
Db     301 E 301


RESULT 13
AAW47194
ID   AAW47194 standard; Protein; 301 AA.
XX
AC   AAW47194;
XX
DT   03-JUL-1998  (first entry)
XX
DE   Herpes simplex virus tegument protein VP22.
XX
KW   HSV; tegument protein; VP22; UL49; antiviral agent; treatment;
KW   cold sore; genital herpes; chickenpox; shingles.
XX
OS   Herpes simplex virus.
XX
PN   WO9804708-A1.
```

```
XX
PD   05-FEB-1998.
XX
PF   28-JUL-1997;   97WO-GB02036.
XX
PR   26-JUL-1996;   96GB-0015726.
XX
PA   (MEDI-) MEDICAL RES COUNCIL.
XX
PI   Hope RG,  McGeoch DJ,  McLaughlan J,  Rixon HWM;
XX
DR   WPI; 1998-130696/12.
DR   N-PSDB; AAV17085.
XX
PT   New antiviral agent disrupting binding of VP22 to VP16 or gB -
PT   useful for treating infections caused by herpes simplex, e.g. cold
PT   sores and chicken-pox
XX
PS   Example; Pages 49-50; 75pp; English.
XX
CC   The present sequence is the herpes simplex virus (HSV)
CC   tegument protein VP22. VP22 was used in the preparation of a novel
CC   antiviral agent, which inhibits the maturation and/or replication
CC   of HSV by disrupting association between VP22 and VP16 and/or gB.
CC   The agent can be used to treat, e.g. cold sores, genital herpes,
CC   chickenpox and shingles.
XX
SQ   Sequence   301 AA;

  Query Match             99.5%;  Score 1553;  DB 19;  Length 301;
  Best Local Similarity   99.7%;  Pred. No. 3e-121;
  Matches  300;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MTSRRSVKSGPREVPRDEYEDLYYTPSSGMASPDSPPDTSRRGALQTRSRQRGEVRFVQY 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MTSRRSVKSGPREVPRDEYEDLYYTPSSGMASPDSPPDTSRRGALQTRSRQRGEVRFVQY 60

Qy      61 DESDYALYGGSSSEDDEHPEVPRTRRPVSGAVLSGPGPARAPPPPAGSGGAGRTPTTAPR 120
           |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db      61 DESDYALYGGSSSEDDEQPEVPRTRRPVSGAVLSGPGPARAPPPPAGSGGAGRTPTTAPR 120

Qy     121 APRTQRVATKAPAAPAAETTRGRKSAQPESAALPDAPASTAPTRSKTPAQGLARKLHFST 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 APRTQRVATKAPAAPAAETTRGRKSAQPESAALPDAPASTAPTRSKTPAQGLARKLHFST 180

Qy     181 APPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAVQLWDMSRPRTDEDLNELLGITT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 APPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAVQLWDMSRPRTDEDLNELLGITT 240

Qy     241 IRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSAASRPTERPRAPARSASRPRRPV 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 IRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSAASRPTERPRAPARSASRPRRPV 300

Qy     301 E 301
           |
Db     301 E 301


RESULT 14
AAY83261
ID   AAY83261 standard; Protein; 301 AA.
XX
AC   AAY83261;
XX
DT   16-AUG-2000  (first entry)
XX
DE   HSV-1 V22 cellular localisation signal sequence.
XX
KW   Ubiquitin ligase; SCF; F-box protein; targeted degradation;
KW   destabilisation; proteolysis; drug discovery; gene therapy; cancer;
KW   oncoprotein; Huntington's disease; gene knockout; delivery systems.
XX
OS   Synthetic.
OS   Herpes simplex virus-1.
XX
PN   WO200022110-A2.
XX
PD   20-APR-2000.
XX
PF   08-OCT-1999;   99WO-US23705.
XX
PR   09-OCT-1998;   98US-0103787.
XX
PA   (HARD ) HARVARD COLLEGE.
XX
PI   Zhou P,  Howley P;
XX
DR   WPI; 2000-317970/27.
DR   N-PSDB; AAZ93717.
XX
PT   Targeting degradation of polypeptide useful for treating cancer and
PT   other proliferative disorders, involves conjugating polypeptide with
PT   ubiquitin protein ligase or inhibiting ubiquitination using organic
PT   compound
XX
PS   Disclosure; Page 76; 185pp; English.
XX
CC   The F-box proteins are a family of ubiquitin ligases (SCF ubiquitin
CC   ligases) which can be used for the targetted degradation of a target
CC   polypeptide in vivo. Targetted degradation is achieved by expressing
CC   the ubiquitin ligase in a cell linked to the interaction domain of
CC   the target polypeptide and thereby recruiting the target polypeptide
CC   to the ubiquitin ligase. Such methods are useful for decreasing or
CC   increasing the level of a target polypeptide and for creating and
CC   expressing a destabilized polypeptide which is subjected to SCF
CC   mediated proteolysis. Degrading any desired protein in a cell is
CC   useful for preventing or treating diseases caused by the presence of
CC   abnormal amount of the specific polypeptides, for drug discovery and
CC   for gene therapy. Diseases treated include cancer, by degradation of
CC   oncoproteins, Huntington's disease, other proliferative disorders and
CC   microbial infections. The method provides a quick and easy
CC   alternative to gene knockout technology. The target polypeptide can
CC   be degraded at all stages, or a specific stage, of development in the
CC   mature animal. The hybrid ubiquitin ligase may also include an
CC   optional localisation sequence such as this HSV-1 V22 sequence.
XX
SQ   Sequence   301 AA;

  Query Match             99.5%;  Score 1553;  DB 21;  Length 301;
  Best Local Similarity   99.7%;  Pred. No. 3e-121;
  Matches  300;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MTSRRSVKSGPREVPRDEYEDLYYTPSSGMASPDSPPDTSRRGALQTRSRQRGEVRFVQY 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MTSRRSVKSGPREVPRDEYEDLYYTPSSGMASPDSPPDTSRRGALQTRSRQRGEVRFVQY 60

Qy      61 DESDYALYGGSSSEDDEHPEVPRTRRPVSGAVLSGPGPARAPPPPAGSGGAGRTPTTAPR 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 DESDYALYGGSSSEDDEHPEVPRTRRPVSGAVLSGPGPARAPPPPAGSGGAGRTPTTAPR 120

Qy     121 APRTQRVATKAPAAPAAETTRGRKSAQPESAALPDAPASTAPTRSKTPAQGLARKLHFST 180
           |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db     121 APRTQRVATKAPAAAAAETTRGRKSAQPESAALPDAPASTAPTRSKTPAQGLARKLHFST 180

Qy     181 APPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAVQLWDMSRPRTDEDLNELLGITT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 APPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAVQLWDMSRPRTDEDLNELLGITT 240

Qy     241 IRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSAASRPTERPRAPARSASRPRRPV 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 IRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSAASRPTERPRAPARSASRPRRPV 300

Qy     301 E 301
           |
Db     301 E 301
```

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RESULT 15
AAY96574
ID   AAY96574 standard; Protein; 297 AA.
XX
AC   AAY96574;
XX
DT   12-SEP-2000  (first entry)
XX
DE   HSV-1 VP22 polypeptide.
XX
KW   hEST2; telomerase; catalytic subunit; reverse transcriptase; life-span;
KW   retinoblastoma; p53; tumour suppressor; inhibitor; arteriosclerosis;
KW   proliferation; immortal; tumour therapy; macular degeneration; activator;
KW   INK4; HSV-1; VP22; fusion protein.
XX
OS   Herpes simplex virus 1.
XX
PN   WO200031238-A2.
XX
PD   02-JUN-2000.
XX
PF   24-NOV-1999;   99WO-US27907.
XX
PR   25-NOV-1998;   98US-0109891.
PR   17-FEB-1999;   99US-0120549.
XX
PA   (GENE-) GENETICA INC.
XX
PI   Hannon GJ,  Beach DH;
XX
DR   WPI; 2000-400055/34.
DR   N-PSDB; AAA29395.
XX
PT   New method for increasing the proliferative capacity of cell lines
PT   comprises administering agents reversibly activating telomerase
PT   activity and reversibly inactivating Rb/INk4 and/or p53 pathways useful
PT   in treating age related diseases
XX
PS   Disclosure; Page 31-32; 123pp; English.
XX
CC   The HSV-1 VP22 polypeptide can be fused to a retinoblastoma (Rb)
CC   inactivator protein sequence to aid targeting and internalization.
CC   The invention concerns methods and reagents for extending the life-span,
CC   e.g. the number of mitotic divisions, of a cell. The method relies on
CC   activation of a telomerase activity and inhibition of one or both of a
CC   Rb/INK4 pathway or a p53 pathway. Phosphorylation of Rb by
CC   cyclin-dependent kinases, cdk4 and cdk6, releases the cells into the
CC   division cycle. Binding of INK4 family members, e.g. the tumour
CC   suppressor p16INK4a, inhibits kinase activity and results in growth
CC   arrest. Rb inactivators can selectively and reversibly inactivate an
CC   Rb/INK4 pathway, especially an Rb/p16INK4a pathway. The oncoprotein MDM2
CC   is a cellular inhibitor of Rb/E2F function and the p53 tumour suppressor
CC   and can also be used in the methods. Other molecules which can be used
CC   include cdk4 or cdk6 mutants. In particular, a cdk4 mutant is one which
CC   differs from at one or more of residues K22, R24, H95 and/or D97.
CC   Additional constructs include a papilloma virus E7 protein, or other
CC   viral oncoprotein which bypasses Rb and/or p53. Antisense constructs of
CC   the Rb and p16INK4a genes may also be used. The methods are useful for
CC   increasing the proliferative capacity of cells. The cells are
CC   subsequently of use in pharmaceutical and cosmetic preparations used to
CC   treat conditions related to (premature) ageing, e.g. macular degeneration
CC   and arteriosclerosis. The cells can also be used to replace tumour cell
CC   lines in vitro and for studies on biochemical and physiological aspects
CC   of growth and differentiation. Long lived (immortal) cells could also be
CC   of use in the production of normal or genetically engineered
CC   biotechnology products.
XX
SQ   Sequence   297 AA;

  Query Match             97.4%;  Score 1520;  DB 21;  Length 297;
  Best Local Similarity   98.3%;  Pred. No. 1.6e-118;
  Matches  296;  Conservative    0;  Mismatches    1;  Indels    4;  Gaps    1;

Qy       1 MTSRRSVKSGPREVPRDEYEDLYYTPSSGMASPDSPPDTSRRGALQTRSRQRGEVRFVQY 60
           ||||||||||||||||    ||||||||||||||||||||||||||||||||||||||||
Db       1 MTSRRSVKSGPREVPR----DLYYTPSSGMASPDSPPDTSRRGALQTRSRQRGEVRFVQY 56

Qy      61 DESDYALYGGSSSEDDEHPEVPRTRRPVSGAVLSGPGPARAPPPPAGSGGAGRTPTTAPR 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      57 DESDYALYGGSSSEDDEHPEVPRTRRPVSGAVLSGPGPARAPPPPAGSGGAGRTPTTAPR 116

Qy     121 APRTQRVATKAPAAPAAETTRGRKSAQPESAALPDAPASTAPTRSKTPAQGLARKLHFST 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     117 APRTQRVATKAPAAPAAETTRGRKSAQPESAALPDAPASTAPTRSKTPAQGLARKLHFST 176

Qy     181 APPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAVQLWDMSRPRTDEDLNELLGITT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     177 APPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAVQLWDMSRPRTDEDLNELLGITT 236

Qy     241 IRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSAASRPTERPRAPARSASRPRRPV 300
           ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db     237 IRVTVCEGKNLLQRATELVNPDVVQDVDAATATRGRSAASRPTERPRAPARSASRPRRPV 296

Qy     301 E 301
           |
Db     297 E 297

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GenCore version 5.1.4_p5_4578

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(without alignments)
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1561	100.0	301	3	US-08-303-861-21	Sequence 21, Appl
2	1561	100.0	301	4	US-09-011-073A-1	Sequence 1, Appli
3	1554	99.6	301	4	US-09-347-504-12	Sequence 12, Appl
4	1548	99.2	301	4	US-09-230-421-2	Sequence 2, Appli
5	1203.5	77.1	246	4	US-09-336-093-5	Sequence 5, Appli
6	573	36.7	144	4	US-09-230-421-3	Sequence 3, Appli
7	271.5	17.4	258	3	US-08-303-861-18	Sequence 18, Appl
8	271.5	17.4	258	3	US-08-303-861-19	Sequence 19, Appl
9	271.5	17.4	258	4	US-09-213-343-2	Sequence 2, Appli
10	225.5	14.4	302	3	US-08-303-861-20	Sequence 20, Appl
11	179	11.5	37	4	US-09-347-504-14	Sequence 14, Appl
12	172.5	11.1	139	1	US-08-680-726A-66	Sequence 66, Appl
13	172.5	11.1	139	4	US-09-092-409-66	Sequence 66, Appl
14	169	10.8	34	4	US-09-011-073A-2	Sequence 2, Appli
15	166	10.6	32	4	US-09-230-421-14	Sequence 14, Appl
16	142.5	9.1	263	5	PCT-US91-06532-2	Sequence 2, Appli
17	141	9.0	258	4	US-08-483-533-26	Sequence 26, Appl
18	141	9.0	258	4	US-09-283-471A-26	Sequence 26, Appl
19	141	9.0	264	4	US-08-483-533-40	Sequence 40, Appl
20	141	9.0	264	4	US-09-283-471A-40	Sequence 40, Appl
21	136.5	8.7	355	4	US-08-483-533-41	Sequence 41, Appl
22	136.5	8.7	355	4	US-09-283-471A-41	Sequence 41, Appl
23	136.5	8.7	355	5	PCT-US91-06532-3	Sequence 3, Appli
24	131.5	8.4	661	2	US-08-795-868-14	Sequence 14, Appl
25	131.5	8.4	661	4	US-09-303-069-14	Sequence 14, Appl
26	131.5	8.4	661	4	US-09-134-250-14	Sequence 14, Appl
27	130.5	8.4	591	3	US-09-082-737-2	Sequence 2, Appli
28	129.5	8.3	252	4	US-08-483-533-43	Sequence 4
29	129.5	8.3	252	4	US-09-283-471A-43	Sequence 43, Appl
30	128	8.2	882	4	US-09-413-814-78	Sequence 78, Appl
31	127.5	8.2	404	4	US-09-232-468A-8	Sequence 8, Appli
32	126.5	8.1	1298	2	US-08-690-473-2	Sequence 2, Appli
33	126.5	8.1	1298	4	US-09-259-821A-2	Sequence 2, Appli
34	126.5	8.1	1298	4	US-08-843-659-2	Sequence 2, Appli
35	122	7.8	265	4	US-09-199-637A-369	Sequence 369, App
36	120.5	7.7	941	4	US-07-757-022B-14	Sequence 14, Appl
37	120.5	7.7	1022	4	US-07-757-022B-84	Sequence 84, Appl
38	120.5	7.7	1038	4	US-07-757-022B-74	Sequence 74, Appl
39	120.5	7.7	1049	4	US-07-757-022B-58	Sequence 58, Appl
40	120.5	7.7	1140	4	US-07-757-022B-104	Sequence 104, App
41	120.5	7.7	1270	4	US-07-757-022B-44	Sequence 44, Appl
42	120.5	7.7	1311	4	US-07-757-022B-42	Sequence 42, Appl
43	120.5	7.7	1313	4	US-07-757-022B-142	Sequence 142, App
44	120.5	7.7	1314	4	US-07-757-022B-50	Sequence 50, Appl
45	120.5	7.7	1320	4	US-07-757-022B-46	Sequence 46, Appl

ALIGNMENTS

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RESULT 1
US-08-303-861-21
; Sequence 21, Application US/08303861
; Patent No. 6086902
;  GENERAL INFORMATION:
;    APPLICANT:  ZAMB, TIMOTHY
;    APPLICANT:  LIANG, XIAOPING
;    APPLICANT:  BABIUK, LORNE A.
;    TITLE OF INVENTION:  RECOMBINANT BOVINE HERPESVIRUS TYPE I
;    TITLE OF INVENTION:  VACCINES
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  755 Page Mill Road
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304-1018
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/303,861
;      FILING DATE:  09-SEP-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  PARK, FREDDIE K.
;      REGISTRATION NUMBER:  35,636
;      REFERENCE/DOCKET NUMBER:  29310-20020.20
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 813-5600
;      TELEFAX:  (415) 494-0792
;      TELEX:  706141
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  301 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-303-861-21

  Query Match           100.0%;  Score 1561;  DB 3;  Length 301;
  Best Local Similarity  100.0%;  Pred. No. 1.5e-127;
  Matches  301;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy      61 DESDYALYGGSSSEDDEHPEVPRTRRPVSGAVLSGPGPARAPPPPAGSGGAGRTPTTAPR 120
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Qy     121 APRTQRVATKAPAAPAAETTRGRKSAQPESAALPDAPASTAPTRSKTPAQGLARKLHFST 180
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Db     121 APRTQRVATKAPAAPAAETTRGRKSAQPESAALPDAPASTAPTRSKTPAQGLARKLHFST 180

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Qy     301 E 301
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Db     301 E 301


RESULT 2
US-09-011-073A-1
; Sequence 1, Application US/09011073A
; Patent No. 6184038
;  GENERAL INFORMATION:
;    APPLICANT:  O'Hare et al.
;    TITLE OF INVENTION:  TRANSPORT PROTEINS AND THEIR USES
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Klarquist Sparkman Campbell Leigh &
;      ADDRESSEE:  Whinston, LLP
;      STREET:  One World Trade Center
;      STREET:  121 S.W. Salmon Street
;      STREET:  Suite 1600
;      CITY:  Portland
;      STATE:  Oregon
;      COUNTRY:  United States of America
;      ZIP:  97204-2988
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Disk, 3-1/2 inch
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  MS DOS
;      SOFTWARE:  WordPerfect 7.0 & ASCII
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,073A
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB96/01831
;      FILING DATE:  JULY 25, 1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Earp, David J.
;      REGISTRATION NUMBER:  41,401
;      REFERENCE/DOCKET NUMBER:  5759-49294/DJE
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (503) 226-7391
;      TELEFAX:  (503) 228-9446
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  301
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-011-073A-1

  Query Match             100.0%;  Score 1561;  DB 4;  Length 301;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-127;
  Matches  301;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy      61 DESDYALYGGSSSEDDEHPEVPRTRRPVSGAVLSGPGPARAPPPPAGSGGAGRTPTTAPR 120
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Qy     121 APRTQRVATKAPAAPAAETTRGRKSAQPESAALPDAPASTAPTRSKTPAQGLARKLHFST 180
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Qy     181 APPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAVQLWDMSRPRTDEDLNELLGITT 240
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Qy     241 IRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSAASRPTERPRAPARSASRPRRPV 300
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Qy     301 E 301
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Db     301 E 301


RESULT 3
US-09-347-504-12
; Sequence 12, Application US/09347504
; Patent No. 6399075
; GENERAL INFORMATION:
;  APPLICANT:  Howley, Peter M.
;  APPLICANT:  Benson, John
;  APPLICANT:  Kasukawa, Hiroaki
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR TREATING
;  TITLE OF INVENTION:  PAPILLOMAVIRUS-INFECTED CELLS
;  FILE REFERENCE:  HMV-041.01
;  CURRENT APPLICATION NUMBER: US/09/347,504
;  CURRENT FILING DATE:  1999-07-02
;  NUMBER OF SEQ ID NOS:  79
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 12
;   LENGTH: 301
;   TYPE: PRT
;   ORGANISM: HSV
;   FEATURE:
;   OTHER INFORMATION: HSV-1 VP22 peptide
US-09-347-504-12

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Db     121 APRTGRVATKAPAAPAAETTRGRKSAQPESAALPDAPASTAPTRSKTPAQGLARKLHFST 180

Qy     181 APPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAVQLWDMSRPRTDEDLNELLGITT 240
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Qy     241 IRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSAASRPTERPRAPARSASRPRRPV 300
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Qy     301 E 301
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Db     301 E 301
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RESULT 4
US-09-230-421-2
; Sequence 2, Application US/09230421
; Patent No. 6200577
; GENERAL INFORMATION:
;  APPLICANT:  Medical Research Council
;  TITLE OF INVENTION:  ANTI-HERPESVIRAL ALENTS AND ASSAYS
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE:  P18189C
;  CURRENT APPLICATION NUMBER: US/09/230,421
;  CURRENT FILING DATE:  1999-01-25
;  NUMBER OF SEQ ID NOS:  14
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 2
;   LENGTH: 301
;   TYPE: PRT
;   ORGANISM: HERPESVIRUS TYPE 1
US-09-230-421-2

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  Best Local Similarity   99.3%;  Pred. No. 2.1e-126;
  Matches  299;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

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Qy      61 DESDYALYGGSSSEDDEHPEVPRTRRPVSGAVLSGPGPARAPPPPAGSGGAGRTPTTAPR 120
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Qy     121 APRTQRVATKAPAAPAAETTRGRKSAQPESAALPDAPASTAPTRSKTPAQGLARKLHFST 180
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Db     121 APRTQRVATKAPAAPAAETTRGRKSAQPESAALPDAPASTAPTRSKTPAQGLARKLHFST 180

Qy     181 APPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAVQLWDMSRPRTDEDLNELLGITT 240
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Db     181 APPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAVQLWDMSRPRTDEALNELLGITT 240

Qy     241 IRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSAASRPTERPRAPARSASRPRRPV 300
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Db     241 IRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSAASRPTERPRAPARSASRPRRPV 300

Qy     301 E 301
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Db     301 E 301


RESULT 5
US-09-336-093-5
; Sequence 5, Application US/09336093A
; Patent No. 6348185
; GENERAL INFORMATION:
;  APPLICANT: Washington University School of Medicine
;  TITLE OF INVENTION: MEMBRANE-PERMEANT PEPTIDE COMPLEXES FOR MEDICAL
;  TITLE OF INVENTION: IMAGING, DIAGNOSTICS, AND PHARMACEUTICAL THERAPY
;  FILE REFERENCE: WSHU 2001
;  CURRENT APPLICATION NUMBER: US/09/336,093A
;  CURRENT FILING DATE: 1999-06-18
;  NUMBER OF SEQ ID NOS: 31
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 246
;   TYPE: PRT
;   ORGANISM: Herpes simplex virus VP22 protein
US-09-336-093-5

  Query Match             77.1%;  Score 1203.5;  DB 4;  Length 246;
  Best Local Similarity   80.7%;  Pred. No. 1e-96;
  Matches  243;  Conservative    0;  Mismatches    3;  Indels   55;  Gaps    2;

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Qy      61 DESDYALYGGSSSEDDEHPEVPRTRRPVSGAVLSGPGPARAPPPPAGSGGAGRTPTTAPR 120
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Qy     121 APRTQRVATKAPAAPAAETTRGRKSAQPESAALPDAPASTAPTRSKTPAQGLARKLHFST 180
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Qy     181 APPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAVQLWDMSRPRTDEDLNELLGITT 240
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Db     164 ----------------------------------VQLWQMSRPRTDEDLNELLGITH 186

Qy     241 IRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSAASRPTERPRAPARSASRPRRPV 300
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Db     187 -RVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSAASRPTERPRAPARSASRPRRPV 245

Qy     301 E 301
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Db     246 E 246


RESULT 6
US-09-230-421-3
; Sequence 3, Application US/09230421
; Patent No. 6200577
; GENERAL INFORMATION:
;  APPLICANT:  Medical Research Council
;  TITLE OF INVENTION:  ANTI-HERPESVIRAL ALENTS AND ASSAYS
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE:  P18189C
;  CURRENT APPLICATION NUMBER: US/09/230,421
;  CURRENT FILING DATE:  1999-01-25
;  NUMBER OF SEQ ID NOS:  14
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 3
;   LENGTH: 144
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC PEPTIDES DERIVED FROM THE VP22TRUNC
;   OTHER INFORMATION: SEQUENCE
US-09-230-421-3

  Query Match             36.7%;  Score 573;  DB 4;  Length 144;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-42;
  Matches  110;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     158 ASTAPTRSKTPAQGLARKLHFSTAPPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAA 217
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Db      22 ASTAPTRSKTPAQGLARKLHFSTAPPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAA 81

Qy     218 VQLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQDV 267
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Db      82 VQLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQDV 131


RESULT 7
US-08-303-861-18
; Sequence 18, Application US/08303861
; Patent No. 6086902
;  GENERAL INFORMATION:
;    APPLICANT:  ZAMB, TIMOTHY
;    APPLICANT:  LIANG, XIAOPING
;    APPLICANT:  BABIUK, LORNE A.
;    TITLE OF INVENTION:  RECOMBINANT BOVINE HERPESVIRUS TYPE I
;    TITLE OF INVENTION:  VACCINES
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
```

```
;      STREET:  755 Page Mill Road
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304-1018
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/303,861
;      FILING DATE:  09-SEP-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  PARK, FREDDIE K.
;      REGISTRATION NUMBER:  35,636
;      REFERENCE/DOCKET NUMBER:  29310-20020.20
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 813-5600
;      TELEFAX:  (415) 494-0792
;      TELEX:  706141
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  258 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-303-861-18

  Query Match             17.4%;  Score 271.5;  DB 3;  Length 258;
  Best Local Similarity   31.2%;  Pred. No. 4.4e-16;
  Matches   81;  Conservative   25;  Mismatches  109;  Indels   45;  Gaps    8;

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Qy     100 RAPPPPAGSG-----GAGRT---PTTAPRAPRTQRVATKAPAAPA-----AETTRGRKSA 146
            |   ||  |      || |   |  ||     : | ::: | | |        |||
Db      63 AAAVQPAARGRDRAAAAGTTVAAPAAAPARRSSSRASSRPPRAAADPPVLRPATRGSSGG 122

Qy     147 QPESAALPDAPASTAPTRSKTPAQGLARKLHFSTAPPNPDAPWTPRVAGFNKRVFCAAVG 206
               |  |  |   ||  :   | |  | | || ||  | |||      :|: :|| ||
Db     123 AGAVAVGP--PRPRAPPGANAVASG--RPLAFSAAPKTPKAPWCGPTHAYNRTIFCEAVA 178

Qy     207 RLAAMHARMAAVQLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQD 266
             :|| :|| ||  :||   |:::| |: :|    ||: |||| ||  ||::      :
Db     179 LVAAEYARQAAASVWDSDPPKSNERLDRMLKSAAIRILVCEGSGLLAAANDILAARAQRP 238

Qy     267 VDAATATRGRSAASRPTERP 286
           : : | |       ||
Db     239 AARGSTSGGESRLRGERARP 258


RESULT 8
US-08-303-861-19
; Sequence 19, Application US/08303861
; Patent No. 6086902
;  GENERAL INFORMATION:
;    APPLICANT:  ZAMB, TIMOTHY
;    APPLICANT:  LIANG, XIAOPING
;    APPLICANT:  BABIUK, LORNE A.
;    TITLE OF INVENTION:  RECOMBINANT BOVINE HERPESVIRUS TYPE I
;    TITLE OF INVENTION:  VACCINES
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  755 Page Mill Road
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304-1018
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/303,861
;      FILING DATE:  09-SEP-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  PARK, FREDDIE K.
;      REGISTRATION NUMBER:  35,636
;      REFERENCE/DOCKET NUMBER:  29310-20020.20
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 813-5600
;      TELEFAX:  (415) 494-0792
;      TELEX:  706141
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  258 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-303-861-19

  Query Match             17.4%;  Score 271.5;  DB 3;  Length 258;
  Best Local Similarity   31.2%;  Pred. No. 4.4e-16;
  Matches   81;  Conservative   25;  Mismatches  109;  Indels   45;  Gaps    8;

Qy      61 DESDY----------ALYGGSSSEDDEHPEVPRTRRPVSGAVLSGPGP----------A 99
           || ||          :||   |  ||   |  |       |  ||| |          :
Db      10 DEDDYEYSDLWVRENSLYDYESGSDDHVYEELR-------AATSGPEPSGRRASVRACAS 62

Qy     100 RAPPPPAGSG-----GAGRT---PTTAPRAPRTQRVATKAPAAPA-----AETTRGRKSA 146
            |   ||  |      || |   |  ||     : | ::: | | |        |||
Db      63 AAAVQPAARGRDRAAAAGTTVAAPAAAPARRSSSRASSRPPRAAADPPVLRPATRGSSGG 122

Qy     147 QPESAALPDAPASTAPTRSKTPAQGLARKLHFSTAPPNPDAPWTPRVAGFNKRVFCAAVG 206
               |  |  |   ||  :   | |  | | || ||  | |||      :|: :|| ||
Db     123 AGAVAVGP--PRPRAPPGANAVASG--RPLAFSAAPKTPKAPWCGPTHAYNRTIFCEAVA 178

Qy     207 RLAAMHARMAAVQLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQD 266
             :|| :|| ||  :||   |:::| |: :|    ||: |||| ||  ||::      :
Db     179 LVAAEYARQAAASVWDSDPPKSNERLDRMLKSAAIRILVCEGSGLLAAANDILAARAQRP 238

Qy     267 VDAATATRGRSAASRPTERP 286
           : : | |       ||
Db     239 AARGSTSGGESRLRGERARP 258


RESULT 9
US-09-213-343-2
; Sequence 2, Application US/09213343
; Patent No. 6316252
; GENERAL INFORMATION:
;  APPLICANT: Harms, Jerome S.
;  APPLICANT: Splitter, Gary A.
;  TITLE OF INVENTION: Biotherapeutic Delivery System
;  FILE REFERENCE: 960296.95564
;  CURRENT APPLICATION NUMBER: US/09/213,343
;  CURRENT FILING DATE: 1998-12-17
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 258
;   TYPE: PRT
;   ORGANISM: Bovine herpesvirus 1
US-09-213-343-2

  Query Match             17.4%;  Score 271.5;  DB 4;  Length 258;
  Best Local Similarity   31.2%;  Pred. No. 4.4e-16;
  Matches   81;  Conservative   25;  Mismatches  109;  Indels   45;  Gaps
```

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Qy      61 DESDY----------ALYGGSSSEDDEHPEVPRTRRPVSGAVLSGPGP----------A 99
           || ||         :||   |  ||   |  |       |  ||| |          :
Db      10 DEDDYEYSDLWVRENSLYDYESGSDDHVYEELR-------AATSGPEPSGRRASVRACAS 62

Qy     100 RAPPPPAGSG-----GAGRT---PTTAPRAPRTQRVATKAPAAPA-----AETTRGRKSA 146
            |   ||  |      || |   |  ||    : | ::: | | |        |||
Db      63 AAAVQPAARGRDRAAAAGTTVAAPAAAPARRSSSRASSRPPRAAADPPVLRPATRGSSGG 122

Qy     147 QPESAALPDAPASTAPTRSKTPAQGLARKLHFSTAPPNPDAPWTPRVAGFNKRVFCAAVG 206
           |  |  |   ||  :   | |  | | || ||  | |||      :|: :|| ||
Db     123 AGAVAVGP--PRPRAPPGANAVASG--RPLAFSAAPKTPKAPWCGPTHAYNRTIFCEAVA 178

Qy     207 RLAAMHARMAAVQLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQD 266
           :|| :|| ||  :||   |:::| |: :|    ||: |||| ||  ||::      :
Db     179 LVAAEYARQAAASVWDSDPPKSNERLDRMLKSAAIRILVCEGSGLLAAANDILAARAQRP 238

Qy     267 VDAATATRGRSAASRPTERP 286
           : : | |       ||
Db     239 AARGSTSGGESRLRGERARP 258


RESULT 10
US-08-303-861-20
; Sequence 20, Application US/08303861
; Patent No. 6086902
;  GENERAL INFORMATION:
;    APPLICANT:  ZAMB, TIMOTHY
;    APPLICANT:  LIANG, XIAOPING
;    APPLICANT:  BABIUK, LORNE A.
;    TITLE OF INVENTION:  RECOMBINANT BOVINE HERPESVIRUS TYPE I
;    TITLE OF INVENTION:  VACCINES
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  755 Page Mill Road
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304-1018
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/303,861
;      FILING DATE:  09-SEP-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  PARK, FREDDIE K.
;      REGISTRATION NUMBER:  35,636
;      REFERENCE/DOCKET NUMBER:  29310-20020.20
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 813-5600
;      TELEFAX:  (415) 494-0792
;      TELEX:  706141
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  302 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-303-861-20

  Query Match             14.4%;  Score 225.5;  DB 3;  Length 302;
  Best Local Similarity   26.2%;  Pred. No. 5.2e-12;
  Matches   89;  Conservative   27;  Mismatches  107;  Indels  117;  Gaps   10;

Qy       2 TSRRSVKSGP--------------REVPRDEYEDLYYTPSSGMASPDSPPDTSRRGALQ 46
           |:|||| ||               : |   | |||:   :       | |:|
Db      29 TARRSVVVGPPDDSDDSLGYITTVGADSPSPVYADLYFEHKNTTPRVHQPNDSS------ 82

Qy      47 TRSRQRGEVRFVQYDESDYALYGGSSSEDDEHPEVPRTRRP-------VSGAVLSGPGPA 99
                                    ||  : ::  ||    |        |  ||   |
Db      83 ----------------------GSEDDFEDIDEVVAAFREARLRHELVEDAVYENPLSV 119

Qy     100 RAPPPPAGSGGAGRTPTTAPRAPRTQRVATKAPAAPAAETTRGRKSAQPESAALPDAPAS 159
             |                        |  ||  |             :|:   | |:|
Db     120 EKP----------------------SRSFTKNAA------------VKPK---LEDSP-K 141

Qy     160 TAPTRSKTPAQGLARKLHFSTAPPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAVQ 219
           ||  :   | |  | : |||||   : |      :|||||| || |:||| |: ||
Db     142 RAPPGAGAIASG--RPISFSTAPKTATSSWCGPTPSYNKRVFCEAVRRVAAMQAQKAAEA 199

Qy     220 LWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANE---------------------- 257
           |: : || : :|: ||    ||:|| || ||:| |||
Db     200 AWNSNPPRNNAELDRLLTGAVIRITVHEGLNLIQAANEADLGEGASVSKRGHNRKTGDLQ 259

Qy     258 --LVNPDVVQDVDAATATRGRSAASRPTERPRAPARSASR 295
           : |  :   |   :        | | | |  ||||||
Db     260 GGMGNEPMYAQVRKPKSRTDTQTTGRITNRSR--ARSASR 297


RESULT 11
US-09-347-504-14
; Sequence 14, Application US/09347504
; Patent No. 6399075
; GENERAL INFORMATION:
;  APPLICANT:  Howley, Peter M.
;  APPLICANT:  Benson, John
;  APPLICANT:  Kasukawa, Hiroaki
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR TREATING
;  TITLE OF INVENTION:  PAPILLOMAVIRUS-INFECTED CELLS
;  FILE REFERENCE:  HMV-041.01
;  CURRENT APPLICATION NUMBER: US/09/347,504
;  CURRENT FILING DATE:  1999-07-02
;  NUMBER OF SEQ ID NOS:  79
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 14
;   LENGTH: 37
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: VP22
;   OTHER INFORMATION: (C-terminal domain) peptide
US-09-347-504-14

  Query Match             11.5%;  Score 179;  DB 4;  Length 37;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-09;
  Matches   36;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     266 DVDAATATRGRSAASRPTERPRAPARSASRPRRPVE 301
           |||||||||||||||||||||||||||||||||||||
Db       2 DVDAATATRGRSAASRPTERPRAPARSASRPRRPVE 37


RESULT 12
US-08-680-726A-66
; Sequence 66, Application US/08680726A
; Patent No. 5804197
;  GENERAL INFORMATION:
;    APPLICANT:  Haanes, Elizabeth J.
;    APPLICANT:  Frank, Rexann S.
;    TITLE OF INVENTION:  RECOMBINANT CANINE HERPESVIRUSES
;    NUMBER OF SEQUENCES:  92
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sheridan Ross & McIntosh
;      STREET:  1700 Lincoln Street, Suite 3500
;      CITY:  Denver
;      STATE:  Colorado
;      COUNTRY:  U.S.A.
;      ZIP:  80203
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
```

```
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/680,726A
;      FILING DATE:  12-JUL-1996
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Connell, Gary J.
;      REGISTRATION NUMBER:  32,020
;      REFERENCE/DOCKET NUMBER:  2618-46-C1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (303) 863-9700
;      TELEFAX:  (303) 863-0223
;  INFORMATION FOR SEQ ID NO:  66:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  139 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-680-726A-66

  Query Match             11.1%;  Score 172.5;  DB 1;  Length 139;
  Best Local Similarity   35.0%;  Pred. No. 7.4e-08;
  Matches   43;  Conservative   20;  Mismatches   47;  Indels   13;  Gaps    3;

Qy     178 FSTAPPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAVQLWDMSRPRTDEDLNELLG 237
           ||  |  |  ||      :|| ||| || | |: ||  ||  :||:: |:::|:| : |
Db      20 FSNTPKTPKFPWYGATHLYNKNVFCEAVRRCASKHAIEAASSIWDLNPPQSNEELEKFLT 79

Qy     238 ITTIRVTVCEGKNLLQRANE--LVNPDVVQDVDAATATRGRSAASRPTERPRAPARSASR 295
             ||:|: ||  :|: ||        ||      : :| :||     |: ::| ||
Db      80 KAVIRITISEGLGILKTANTPFSCGQKTADDV------KFKSHSSR-----RSKSQSRSR 128

Qy     296 PRR 298
           |
Db     129 HSR 131


RESULT 13
US-09-092-409-66
; Sequence 66, Application US/09092409
; Patent No. 6159478
;  GENERAL INFORMATION:
;    APPLICANT:  Haanes, Elizabeth J.
;    APPLICANT:  Frank, Rexann S.
;    TITLE OF INVENTION:  RECOMBINANT CANINE HERPESVIRUSES
;    NUMBER OF SEQUENCES:  92
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sheridan Ross & McIntosh
;      STREET:  1700 Lincoln Street, Suite 3500
;      CITY:  Denver
;      STATE:  Colorado
;      COUNTRY:  U.S.A.
;      ZIP:  80203
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/092,409
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/680,726
;      FILING DATE:  12-JUL-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Connell, Gary J.
;      REGISTRATION NUMBER:  32,020
;      REFERENCE/DOCKET NUMBER:  2618-46-C1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (303) 863-9700
;      TELEFAX:  (303) 863-0223
;  INFORMATION FOR SEQ ID NO:  66:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  139 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-092-409-66

  Query Match             11.1%;  Score 172.5;  DB 4;  Length 139;
  Best Local Similarity   35.0%;  Pred. No. 7.4e-08;
  Matches   43;  Conservative   20;  Mismatches   47;  Indels   13;  Gaps    3;

Qy     178 FSTAPPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAVQLWDMSRPRTDEDLNELLG 237
           ||  |  |  ||      :|| ||| || | |: ||  ||  :||:: |:::|:| : |
Db      20 FSNTPKTPKFPWYGATHLYNKNVFCEAVRRCASKHAIEAASSIWDLNPPQSNEELEKFLT 79

Qy     238 ITTIRVTVCEGKNLLQRANE--LVNPDVVQDVDAATATRGRSAASRPTERPRAPARSASR 295
             ||:|: ||  :|: ||        ||      : :| :||     |: ::| ||
Db      80 KAVIRITISEGLGILKTANTPFSCGQKTADDV------KFKSHSSR-----RSKSQSRSR 128

Qy     296 PRR 298
           |
Db     129 HSR 131


RESULT 14
US-09-011-073A-2
; Sequence 2, Application US/09011073A
; Patent No. 6184038
;  GENERAL INFORMATION:
;    APPLICANT:  O'Hare et al.
;    TITLE OF INVENTION:  TRANSPORT PROTEINS AND THEIR USES
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Klarquist Sparkman Campbell Leigh &
;      ADDRESSEE:  Whinston, LLP
;      STREET:  One World Trade Center
;      STREET:  121 S.W. Salmon Street
;      STREET:  Suite 1600
;      CITY:  Portland
;      STATE:  Oregon
;      COUNTRY:  United States of America
;      ZIP:  97204-2988
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Disk, 3-1/2 inch
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  MS DOS
;      SOFTWARE:  WordPerfect 7.0 & ASCII
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,073A
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB96/01831
;      FILING DATE:  JULY 25, 1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Earp, David J.
;      REGISTRATION NUMBER:  41,401
;      REFERENCE/DOCKET NUMBER:  5759-49294/DJE
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (503) 226-7391
;      TELEFAX:  (503) 228-9446
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  34
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-011-073A-2

  Query Match             10.8%;  Score 169;  DB 4;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-08;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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```
Qy    268 DAATATRGRSAASRPTERPRAPARSASRPRRPVE 301
          |||||||||||||||||||||||||||||||||
Db      1 DAATATRGRSAASRPTERPRAPARSASRPRRPVE 34


RESULT 15
US-09-230-421-14
; Sequence 14, Application US/09230421
; Patent No. 6200577
; GENERAL INFORMATION:
;  APPLICANT:  Medical Research Council
;  TITLE OF INVENTION:  ANTI-HERPESVIRAL ALENTS AND ASSAYS
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE:  P18189C
;  CURRENT APPLICATION NUMBER: US/09/230,421
;  CURRENT FILING DATE:  1999-01-25
;  NUMBER OF SEQ ID NOS:  14
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 14
;   LENGTH: 32
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC PEPTIDES DERIVED FROM THE VP22TRUNC
;   OTHER INFORMATION: SEQUENCE
US-09-230-421-14

  Query Match             10.6%;  Score 166;  DB 4;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 4.1e-08;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    190 TPRVAGFNKRVFCAAVGRLAAMHARMAAVQLW 221
          ||||||||||||||||||||||||||||||||
Db      1 TPRVAGFNKRVFCAAVGRLAAMHARMAAVQLW 32


Search completed: May 21, 2003, 17:38:37
Job time : 26.7613 secs
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